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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 16, 2004, 01:12:56 ; Search time 1977 Seconds
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Perfect score: 13215
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Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES
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ALIGNMENTS

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; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-Cepton Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; PRIOR FILING DATE: 2003-04-14
; PRIOR FILING DATE: 2003-04-14
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 7554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-414-692-14

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

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Qy 1081 GlyHisProLeuProLeuGlyLeuHisAspThrAlaArgProValLeuProArgProPro 1100
Db 3241 GGTCAACCACTGGCCCTGGGCTCCATGACACTGCCCGCGCGCTTCTGCGCGCCACCC 3300
Qy 1101 ThrIleSerAsnProProProLeuIleSerSerAlaLysHisProSerValLeuGluArg 1120
Db 3301 ACCATCTCAACCGCGCTCCCTCATCTCTCTGCGCAAGCACCCCGCGCTTCTCGAGG 3360
Qy 1121 GlnIleGlyAlaIleSerGlnGlyMetSerValGlnLeuHisValProTyrSerGluHis 1140
Db 3361 CAATAGGTGCCATCTCTCCCAAGGAATGTGGTCCAGCTCCAGTCCCGCTCTAGAGCAT 3420
Qy 1141 AlaLysAlaProValGlyProValThrMetGlyLeuProLeuProMetAspProLysLys 1160

Db	3421	GCCAAGGCGCGGTGGCGCCCTGTACCATGGCGCTGCCCTCCCATGGACCCCAAAAG	4501	CGTGCTGTCTACGAGGAGAGCCTGAAGAGCGCGCCAGGACCGCCAGCAGCTCGGGGGG
Qy	1161	LeuAlaProPheSerGlyValLysGlnLeuSerProArgGlyGlnAlaGlyPro	1521	SerIleAlaArgGlyAlaProValIleValProGluLeuGlyLysProArgGlnSerPro
Db	3481	CTGGCACCTTACGGGAGTGAAGCAGGAGCAGCTGTCTCCACCGGGCCAGGCTGGGCA	4561	TCCATTGCGCGCGCGCGCGCGCTATTTGCTGAGCTGGGTAAAGCGCGGACAGACCCC
Qy	1181	ProGluSerLeuGlyValProThrAlaGlnGluAlaSerValLeuArgGlyThrAlaLeu	1541	LeuThrTyrGluAspHisGlyAlaProPheAlaGlyHisLeuProArgGlySerProVal
Db	3541	CCGGAGAGCCTGGGGTGCCACAGCCAGGAGCGCTCGGTGAGAGGGACAGCTCTG	4621	CTGACCTATGAGGACCAACGGGCGACCTTTGCGCGCCACCTCCACGAGGTTCCGCGTG
Qy	1201	GlySerValProGlyLysSerIleThrLysGlyIleProSerThrArgValProSerAsp	1561	ThrMetArgGluProThrProArgLeuGlnGluGlySerLeuSerSerSerLysAlaSer
Db	3601	GGCTCAGTTCCGGCGGAGCATCACAAAGGATTCACAGACACGGGTGCCCTCGAC	4681	ACCATGGGGAGCCACCGCGCTTCAGAGAGGCGAGCCTTTCTGCACAGAGCATCC
Qy	1221	SerAlaIleThrTyrArgGlySerIleThrHisGlyThrProAlaAspValLeuTyrLys	1581	GlnAspArgLysLeuThrSerThrProArgGluIleAlaLysSerProHisSerThrVal
Db	3661	AGGCCATCATACCGCGCTCCATCACCCAGCGCACCGCAGCTGACGTCTGTACAAAG	4741	CAGACCGAAAGCTGACGTGACGCTCGTGGAGCTCGCAAGTCCCAAGTCCCGCACAGC
Qy	1241	GlyThrIleThrArgIleIleGlyLeuAspSerProSerArgLeuAspArgGlyArgGlu	1601	ProGluHisHisProHisProIleSerProTyrGluHisLeuLeuArgGlyValSerGly
Db	3721	GGCACCATCACAGGATCATCGCGAGACAGCCGAGTCTGTGGACCCGCGCGGAG	4801	CCCGAGCACCAACCCACACCCCATCTCGCCCTATGAGCACCTGCTTCGGGGCGTGAGTGGC
Qy	1261	AspSerLeuProLysGlyHisValIleTyrGluGlyLysGlyHisValLeuSerTyr	1621	ValAspLeuTyrArgSerHisIleProLeuAlaPheAspProThrSerIleProArgGly
Db	3781	GACAGCTTGCACAGGCGCCAGCTCATCTACGAAGGCAGAGGCGCCACCGTCTGTCTAT	4861	GTGGACCTGTATCGGAGCCACATCCCTCTGGCTTCGACCCACCTCCATACCCCGGGC
Qy	1301	GluGlyGlyMetSerValThrGlnCysSerLysGluAspGlyArgSerSerGlyPro	1641	IleProLeuAspAlaAlaAlaTyrTyrLeuProArgHisLeuAlaProAsnProThr
Db	3841	GAGGTGGCATGTCTGTGACCATCTCAAGGAGGACGGCAGAGCAGCTCAGGACCC	4921	ATCCCTCTGGAGCGAGCGCTGCTTACTACCTGCGCGCACCTGGCGCCCAACCCACCC
Qy	1320	ProHisGluThrAlaAlaProLysArgThrTyrAspMetMetGluGlyArgValGlyArg	1661	TyrProHisLeuTyrProProTyrIleuIleArgGlyTyrProAspThrAlaAlaLeuGlu
Db	3901	CCCCATGAGCGCGCGCCCAAGCGCATCTATGACATGATGAGGGCCCGCTGGGAGA	4981	TACCGCGCATCTGATCCACCCCTTACCTCATCCGCGCTACCCCGACACGCGCGCGCTGGAG
Qy	1340	AlaIleSerSerAlaSerIleGluLeuMetGlyArgAlaIleProProGluArgHis	1700	AsnArgGlnThrIleIleAsnAspTyrIleThrSerGlnGlnMetHisHisAsnThrAla
Db	3961	GCAATCTCTCAGCCAGCATCGAAGTCTCATGGCGCTGTCATCCCGCGGAGCGACAC	5041	AAACCGGACGACCATCATCAATGACTACATCACTCGCAGCAGATGCACACACACGCGCC
Qy	1360	SerProHisHisLeuLysGluGlnHisIleArgGlySerIleThrGlnGlyIlePro	1720	ThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeuSerProArgGluSerSerLeu
Db	4021	AGCCCCACCACTCAAGAGCAGCACCATCCCGCGGTCCATCACACAGGATCCCT	5101	ACCGCATGGCGCAGCGAGCTGATATGTGAGGGGCGCTTCGCGCCCGGAGTCTCGCTG
Qy	1380	ArgSerTyrValGluAlaGlnAspTyrLeuArgArgGluAlaLysLeuLeuLysArg	1740	AlaLeuAsnTyrAlaAlaGlyProArgGlyIleIleAspLeuSerGlnValProHisLeu
Db	4081	CGGTCTCAGTGAGGACAGGAGCTACTCTGCTCGGAGGCCAAGCTCTTAAAGCGG	5161	GCACTCAATACGTCGCGGTCCCGAGGCATCATCGACCTGTCCCAAGTGCCACACCTG
Qy	1400	GluGlyThrProProProProSerArgAspLeuThrGluAlaTyrLysThrGln	1760	ProValLeuValProProThrProGlyThrProAlaThrAlaMetAspArgLeuAlaTyr
Db	4141	GAGGCGACGCTCCGCCCCACCGCCCTCAGCGGACCTGACCGAGGCTTACAGACGCGAG	5221	CCTGTCTCTGTGCCCCCGACACAGCGACCCCGAGCACCGCATGGACCGCTTGCCTAC
Qy	1420	AlaLeuGlyProLeuLysLeuLysProAlaHisGluGlyLeuValAlaThrValLysGlu	1780	LeuProThrAlaProGlnProPheSerSerArgHisSerSerSerProLeuSerProGly
Db	4201	GCCTTGGGCCCCCTGAAGCTGAAGCGCGCCCATGAGGCGCTGTGTGGCCACCGTGAAGGAG	5340	CTCCCGACCGCGCCCGAGCCCTTCAGACCGCGCCACAGCAGCTCCCACTCTCCCGAGA
Qy	1440	AlaGlyArgSerIleHisGluIleProArgGluLeuArgHisThrProGluLeuPro	1800	GlyProThrHisLeuThrLysProThrThrThrSerSerSerGluArgGluArgAspArg
Db	4261	GCGGCGCGCTCCATCATGAGATCCGCGGAGGAGCTCGGCGACACACCGCGAGTGCCT	5400	GGTCCACACACCTTGACAAACCAACACCACTCTCTGCGAGCGGAGCGAGACCGG
Qy	1441	LeuAlaProArgProLeuLysGluGlySerIleThrGlnGlyThrProLeuLysTyrAsp	1820	AspArgGluArgAspArgAspArgGluArgGluLysSerIleLeuThrSerThrThrThr
Db	4321	CTGGCCCCCGCGCTCAAGAGGGCTCCATCACGCGAGGGACCCCGCTCAAGTACGAC	5460	GATCGAGAGCGGACCGGGATCGGAGCGGGAAGTCCATCTCTACGTCCACCGACG
Qy	1461	ThrGlyAlaSerThrThrGlySerLysHisAspValArgSerLeuIleGlySerPro	1840	ValGluHisAlaProIleTyrArgProGlyThrGluGlnSerSerSerGlySerSerGlySer
Db	4381	ACCGCGCGCTCCACCTGGCTCCAAAGACGACGAGTACGCTCCCTCATCGGACGCCCC	5520	GTGGAGCACCGACCATCTCGAGACCTGGTACAGACGAGCAGCAGCGGACGCGCAGC
Qy	1481	GlyArgThrPheProValHisProLeuAspValMetAlaAspAlaArgAlaLeuGlu	1860	SerGlyGlyGlyGlyGlySerSerArgProAlaSerHisSerHisAlaHisGlnHis
Db	4441	GGCCGAGCGTTCCACCCCGTGACCGCTGGATGTGTGATGGCGCGCGCGGACATGGAA	5580	AGCGCGCGGCTGGGGCAGCAGCAGCGCGCGCGCTCCACCTCCCATGCTCCACCGAC
Qy	1501	ArgAlaCysTyrGluGluSerLeuLysSerArgProGlyThrAlaSerSerGlyGly	1880	SerProIleSerProArgThrGlnAspAlaLeuGlnGlnArgProSerValLeuHisAsn
		TCCGCCATCTCTCCCTCGGACCCAGGATGCCCTCCAGCAGAGACCCAGTGTGCTTCAAC	5640	TCCGCCATCTCTCCCTCGGACCCAGGATGCCCTCCAGCAGAGACCCAGTGTGCTTCAAC


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QY 1881 ThrGlyMetLysGlyIleIleThrAlaValGluProSerLysProThrValLeuArgSer 1900
DB 5641 ACAGGCATGAAGGGTATCATCCGCTGTGGAGCCAGCAAGCCACGGTCTCTGAGTCC 5700
QY 1901 ThrSerThrSerSerProValArgProAlaAlaThrPheProProAlaThrHisCysPro 1920
DB 5701 ACCTCCACCTCTCACCCGTTCCGCCAGCTGCCACATTCACACTGCCACCACTGCCCA 5760
QY 1921 LeuGlyGlyThrLeuAspGlyValTyrProThrLeuMetGluProValLeuLeuProLys 1940
DB 5761 CTGGCGGGCACCTTCGATGGGGTCTACCTTACCCTCATGGAGCCCGTCTTGTCTGCCAAG 5820
QY 1941 GluAlaProArgValAlaAlaArgProGluArgProArgAlaAspThrGlyHisAlaPheLeu 1960
DB 5821 GAGGCCCCCGGGTCCGCGCCGAGAGCGGCCCGAGCAGACACCGGCCCATGCTTCTCTC 5880
QY 1961 AlaLysProProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGlu 1980
DB 5881 GCCAAGCCCCCAGCCCGCTCCGGGCTGGAGCCCGCTCTCTCCCCAGCAAGGGCTCGGAG 5940
QY 1981 ProArgProLeuValProProValSerGlyHisAlaThrIleAlaArgThrProAlaLys 2000
DB 5941 CCCCGGCCCTAGTGCCTCTGCTCTGGCCAGCCACCATCGCCCGCACCTTCCGGAAG 6000
QY 2001 AsnLeuAlaProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAsp 2020
DB 6001 AACTCGCACCTCACCCAGCCAGCCCGGACCCCGCGGCCACCTGCTCGGCTCGGAC 6060
QY 2021 ProHisArgGlyLysThrGlnSerLysProPheSerIleGlnGluLeuGluLeuArgSer 2040
DB 6061 CCGCACCGGGAAGAAGCTCAAGTAAACCTTTTCCATCCAGGAACCTGGAACCTCCGTTCT 6120
QY 2041 LeuGlyTyrHisGlySerSerTyrSerProGluGlyValGluProValSerProValSer 2060
DB 6121 CTGGGTTTACACCGCAGCAGCTACAGCCCGGAGGGGTGGAGCCCGTACGCTCTGTGAGC 6180
QY 2061 SerProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluLeuLeuAspLysSer 2080
DB 6181 TCACCCAGTCTGACCCACGACAGAGGGCTCCCCAGACACCTGGAGAGCTCGACAGAGC 6240
QY 2081 HisLeuGluGlyGluLeuArgProLysGlnProGlyProValLysLeuGlyGlyGluAla 2100
DB 6241 CACTTGAGGGGGAGCTGCGGCCCAAGCAGCAGCCCGCTGGAAGCTTGGCGGGAGGCC 6300
QY 2101 AlaHisLeuProHisLeuArgProLeuProGluSerGlnProSerSerSerProLeuLeu 2120
DB 6301 GCCACCTTCCACACTGCGCGCGCTGCTGAGAGCCAGCCCTGCTGCTGAGCCCGCTGCTC 6360
QY 2121 GlnThrAlaProGlyValLysGlyHisGlnArgValValThrLeuAlaGlnHisIleSer 2140
DB 6361 CAGACCCCGCCAGGGGTCAAGGTACACAGGGGTGTACCTTGGCCAGCACATCAGT 6420
QY 2141 GluValIleThrGlnAspTyrThrArgHisIleProGlnGlnLeuSerAlaProLeuPro 2160
DB 6421 GAGGTATCATCAGAGGACTACCCCGGCACACCCAGCAGCTCAGCGCACCCCTGCC 6480
QY 2161 AlaProLeuTyrSerPheProGlyAlaSerCysProValLeuAspLeuArgProPro 2180
DB 6481 GCCCCCTCTACTCTTCTTCCGCGCCAGCTGCCCCGCTCTGGACCTCCCGCGCCACCC 6540
QY 2181 SerAspLeuTyrLeuProProProAspHisGlyAlaProAlaArgGlySerProHisSer 2200
DB 6541 AGTGACCTTACTTCCCGCCCCCGGACGTCGTCGCGCGCTGGCTCCCCCAGCAGC 6600
QY 2201 GluGlyGlyLysArgSerProGluProAsnLysThrSerValLeuGlyGlyGluAsp 2220
DB 6601 GAAGGGGCAAGAGTCTCCAGAGCCCAACAAGACGTCGCTTGGGTGGTGGTGGAGC 6660
QY 2221 GlyIleGluProValSerProProGluGlyMetThrGluProGlyHisIleSerArgSerAla 2240
DB 6661 GGTATTAGACTGTGTCTCCCAACCGGAGGATGACGAGCCAGGCGCACTCCCGAGTGTCT
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QY 2241 ValTyrProLeuLeuTyrArgAspGlyGluGlnThrGluProSerArgMetGlySerLys 2260
DB 6721 GTGTACCCGCTGTGTACCGGATGGGAAACAGACGAGCCAGGATGGGTCCCAAG 6780
QY 2261 SerProGlyAsnThrSerGlnProProAlaPheSerLysLeuThrGluSerAsnSer 2280
DB 6781 TCTCCAGGCAACACCAAGCCAGCCGCGAGCTTCTTACGCAAGCTGACCGAGACACTCC 6840
QY 2281 AlaMetValLysSerLysGlnGluIleAsnLysLysLeuAsnThrHisAsnArgAsn 2300
DB 6841 GCCATGTCAGTCCCAAGAGCAAGAGATCAACAAGAAGCTGAACACCCACCGGAAT 6900
QY 2301 GluProGluTyrAsnIleSerGlnProGlyThrGluIlePheAsnMetProAlaIleThr 2320
DB 6901 GAGCTGAATACATATATCAGCAGCTGGGACGAGATCTTCAATATATGCGCGCATCACC 6960
QY 2321 GlyThrGluLeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMet 2340
DB 6961 GGAAACAGGCTTATGACCTATAGAAGCCAGCGGTGAGGAACATGCCAGCACCAATG 7020
QY 2341 GlyLeuGluAlaIleIleArgLysAlaLeuMetGlyLysTyrAspGlnTyrGluGluSer 2360
DB 7021 GGCTGGAGGCCATATTAGAAAGGCATCTCATGGTAAATATGACCAAGTGGGAAGTCC 7080
QY 2361 ProProLeuSerAlaAsnAlaPheAsnProLeuAsnAlaSerAlaSerLeuProAlaAla 2380
DB 7081 CCGCCGCTCAGCGCCCAATGCTTTTAAACCTCTGAATGCCAGTGCAGCTGCCGCTGCT 7140
QY 2381 MetProIleThrAlaAlaAspGlyArgSerAspHisThrLeuThrSerProGlyGlyGly 2400
DB 7141 ATGCCCATTAACCGCTGCTGACGACGGAGTGACACACACTCCTCGCAGGTGGCGGC 7200
QY 2401 GlyLysAlaLysValSerGlyArgProSerSerArgLysAlaLysSerProAlaProGly 2420
DB 7201 GGAAAGGCCAAGTCTCTGGCAGACCCAGCAGCCGAAAGCCAAAGTCCCGGCCCGGCG 7260
QY 2421 LeuAlaSerGlyAspArgProProSerValSerSerValHisSerGluGlyAspCysAsn 2440
DB 7261 CTGGCATCTGGGACCGGCCACCTCTGCTCTCTCTCAGTCAGTCCGAGGGAGACTGCAAC 7320
QY 2441 ArgArgThrProLeuThrAsnArgValTyrGluAspArgProSerSerAlaGlySerThr 2460
DB 7321 CGCCGAGACCGCTTCAACACCGCTGTGGAGGACAGGCCCTCGTCCGAGGTTCACG 7380
QY 2461 ProPheProTyrAsnProLeuIleMetArgLeuGlnAlaGlyValMetAlaSerProPro 2480
DB 7381 CCATTCCCTTACAAACCCCTGATCATGCGGCTGCAGCGGGGTGTCTGGCTTCCCAACC 7440
QY 2481 ProProGlyLeuProAlaGlySerGlyProLeuAlaGlyProHisIleAlaTyrAspGlu 2500
DB 7441 CCACCGGGCTTCCCGCGGCGCAGCGGGCCCTCGCTGGCCCCCACCACCGCTGGGAGCAG 7500
QY 2501 GluProLysProLeuLeuCysSerGlnTyrGluThrLeuSerAspSerGlu 2517
DB 7501 GAGCCCAAGCACTGCTCTCTCGAGTACGAGACACTCTCCGACAGCAG 7551
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RESULT 2

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US-10-174-014-11
; Sequence 11, Application US/10174014
; Publication No. US20040005292A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
; FILE REFERENCE: PFS-0012
; CURRENT APPLICATION NUMBER: US/10/174,014
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 11
; LENGTH: 8561
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(7555)
US-10-174-014-11

Alignment Scores:
Pred. No.: 0 Length: 8561
Score: 13215.00 Matches: 2517
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-522-753-5 (1-2517) x US-10-174-014-11 (1-8561)

QY 1 MetSerGlySerThrGlnLeuValAlaGlnThrTrpArgAlaThrGluProArgTyrPro 20
DB 2 ATGTGGGGCTCCACACAGCTTGTGGCACAGACGTGGAGGGCCACTGAGCCCGCTACCCG 61
QY 21 ProHisSerLeuSerTyrProValGlnIleAlaArgThrHisThrAspValGlyLeuLeu 40
DB 62 CCCACAGCCCTTTCCTACCCAGTGCAGATGCCCGGAGGCACACGAGCGTCCGGCTCCTG 121
QY 41 GluTyrGlnHisHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleIleGln 60
DB 122 GAGTACCAGCACCACTCCCGCGACTATGCTCCACCTGTCGCGGGCTCCATCATCCAG 181
QY 61 ProGlnArgArgProSerLeuLeuSerGluPheGlnProGlyAsnGluArgSerGln 80
DB 182 CCCACGGGGAGGGCCCTCCCTGCTGCTGAGTTCAGCCCGGGAATGAACGGTCCCAG 241
QY 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
DB 242 GAGCTCCACCTGGCGGCAGAGTCCCACTCATACCTGCCCCAGCTGGGGAAGTCAGAGATG 301
QY 101 GluPheIleGluSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
DB 302 GAGTTCAATCAAGCAAGCCCTCGCTAGAGCTGCTGCTGACCCCTGCTGCGACCG 361
QY 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
DB 362 TCACCCCTGCTGGCCACAGGCCAGCTCGGGAGCTGAAGACCTCACCAAGGACCGTAGC 421
QY 141 LeuThrGlyLysLeuGluProValSerProProSerProHisThrAspProGluLeu 160
DB 422 CTGACGGGCAAGCTGGNACCGGTGTCTCCCCCAGCCCCCGCACACTGACCTGAGCTG 481
QY 161 GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAsnMetAspArgValAsp 180
DB 482 GAGCTGTGCGGCCACCGCTGTCCAGGAGGAGCTGATCCAGAAACATGGACCGCTGGAC 541
QY 181 ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGlnLeu 200
DB 542 CGAGAGATCACCATGTGTAGACGACGAGATCTTAAGCTGAAGAGAAGCAGCAACAGCTG 601
QY 201 GluGluGluAlaAlaLysProGluProGluLysProValSerProProIleGlu 220
DB 602 GAGGAGAGGCTGCCAAGCCGCCGAGCTGAGAGCCCGTGTACCGCGCCCATCGAG 661
QY 221 SerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysLysAlaGluAla 240
DB 662 TCGAAGCACCGCAGCTGTGTGAGATCATCTACGACGAGAACCGGAAGGCTGAAGCT 721
QY 241 AlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGlnPro 260
DB 722 GCACATCGGAATTCGAAGGCCCTGGGGCCCCAGGTGAGCTGCGCTGTACAAACGACCC 781
QY 261 SerAspThrArgGlnTyrHisGluAsnIleLysIleAsnGlnAlaMetArgLysLysLeu 280
DB 782 TCCGACACCCCGGAGTATCATGAGACATCAAAATAAACACGAGCGATGCGGAAGAGCTA 841
QY 281 IleLeuTyrPheLysArgAsnHisAlaArgLysGlnTrpLysGlnLysPheCysGln 300
DB |||||
842 ATCTTGTTACTTCAAGAGGAGGAATCACGCTCGGAAACAATGGAAGCAGAAATTTCTGCCAG 901
QY 301 ArgTyrAspGlnLeuMetGluAlaLeuGluLysValGluArgIleGluAsnAspPro 320
DB 902 CGCTATGACCAGCTCATGGAGGCTTGGAAAAAAGGTGGAGCGCATCGAAAAACAACCCG 961
QY 321 ArgArgArgAlaLysGluSerLysValArgGluTyrTyrGluLysGlnPheProGluIle 340
DB 962 CGCCGGCGGGCCAAAGAGAGCAAGGTGCGCGAGTACTACGAAAGAGCAGTTCCCTGAGATC 1021
QY 341 ArgLysGlnArgGluLeuGlnGluArgMetGlnSerArgValGlyGlnArgGlySerGly 360
DB 1022 CGCAAGCAGCGCGAGCTGCAGAGCGCATGCGAGAGGAGGTGGCGGCGAGCGGGCAGTGG 1081
QY 361 LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluLeuIleLeuAspGlyLeuSer 380
DB 1082 CTGTCCATGTGCGGCCCGCCGACGAGCAGAGGTGTACAGATCATCGATGCGCTCTCA 1141
QY 381 GluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeuTyr 400
DB 1142 GAGCAGGAGAACCTGGAGAGCAGATGCGCCAGCTGCGCGTATCCGCCCATGCTGTAC 1201
QY 401 AspAlaAspGlnGlnArgIleLysPheIleAsnMetAsnGlyLeuMetAlaAspProMet 420
DB 1202 GAGCTGCAGCAGCAGCGCATCAAGTTTCATCAACATGAACGGGCTTATGGCCGACCCATG 1261
QY 421 LysValTyrLysAspArgGlnValMetAsnMetTrpSerGluGlnGluLysGluThrPhe 440
DB 1262 AAGGTGTACAAAGACCGCCAGGTGCATGAACATGTGGAGTGAGCAGGAGAGAGACCTTC 1321
QY 441 ArgGluLysPheMetGlnHisProLysAsnPheGlyLeuIleAlaSerPheLeuGluArg 460
DB 1322 CGGGAGAGTTTCATGACGATCCCAAGAACTTTGGCTGATCGCATCATTTCTTGGAGAG 1381
QY 461 LysThrValAlaGluCysValLeuTyrTyrLeuThrLysLysAsnGluAsnTyrLys 480
DB 1382 AAGACAGTGGCTGAGTGGCTCTCTATTACTACTGAAGAAGAATGAGAACTATAAG 1441
QY 481 SerLeuValArgArgSerTyrArgArgGlyLysSerGlnGlnGlnGlnGlnGln 500
DB 1442 AGCTGTGTGAGACGGAGCTATGCGGCCCGCGGAGAGCCAGCAGCAACAGCAGCAG 1501
QY 501 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 520
DB 1502 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1561
QY 521 AspGluLysGluLysGluLysGluAlaGluLysGluGluLysProGluValGluAsn 540
DB 1562 GATGAGAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1621
QY 541 AspLysGluAspLeuLeuLysGluLysThrAspAspThrSerGlyGluAspAspGlu 560
DB 1622 GACAAAGAGAGACCTCTCAAGGAGAGAGCAGACGACCTCAGGGAGGAGCAACAGCAG 1681
QY 561 LysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSerGlnGlyArgArgLysGly 580
DB 1682 AAGGAGCTGTGGCTTCCAAAGGCCCGCAAACTGCCAACAGCAGCAGGAGAGCAGCAAG 1741
QY 581 ArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluGluAlaIleThrProGlnGln 600
DB 1742 CGCATCACCGCTCAATGGCTAATGAGGCCAACAGCAGGAGGAGGAGGAGGAGGAGGAG 1801
QY 601 SerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArgTrpThrGluGluMet 620
DB 1802 AGCGCCGAGCTGGCTCCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAGAGAAATG 1861
QY 621 GluThrAlaLysLysGlyLeuLeuGluHisGlyArgAsnTrpSerAlaIleAlaArgMet 640
DB 1862 GAAACAGCAAGAAAGGTCTCTGGNACACGCGCCGCACTGGTTCGCGCATCGCCGAGATG 1921
QY 641 ValGlySerLysThrValSerGlnCysLysAsnPheTyrPheAsnTyrLysLysArgGln 660
DB 1922 GTGGGCTCCAAGACTGTGTGCGAGTGTAAAGAACTTCTACTTCAACTACAAGAGAGGCGAG 1981
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Qy	661	AsnLeuAspGluIleLeuGlnGlnHisLysLeuLysMetGluLysGluArgAsnAlaArg	680
Db	1982	AACCTCGATGAGATCTTGCAGCAGCAACAGCTGAAGATGCAGAAGGAGAGAAACGCGCGG	2041
Qy	681	ArgLysLysLysLysAlaProAlaAlaAspSerGluAlaAlaPheProProValVal	700
Db	2042	AGGAAGAAGAGAAGCGCGCGCGCGCGCAGCGAGGAGGCTGCATTCCCGCCGCTGGTG	2101
Qy	701	GluAspGluGluMetGluAlaSerGlyValSerGlyAsnGluGluGluMetValGluGlu	720
Db	2102	GAGATGAGGAGATGGAGGGCTCGGGCGTGAGCGGAATCAGAGGAGATGGTGGAGGAG	2161
Qy	721	AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla	740
Db	2162	GCTGAAGCCTTACATGCTCTCGGGAATGAGTGCACAGAGGGAAATGCAGTGCGCCAGCC	2221
Qy	741	ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaAlaLys	760
Db	2222	ACTGTCAACACACCTCAGACACCGAGAGCATCCCTCTCTCTCACATGAGGCGCGCAAG	2281
Qy	761	AspThrGlyGlnAsnGlyProLysProAlaThrLeuGlyAlaAspGlyProProPro	780
Db	2282	GACACAGGGCAGAAATGGCCCCAAGCCCCCAGCACCTTGGCGCGCAGCGGCCACCCCCA	2341
Qy	781	GlyProProThrProProArgArgThrSerArgAlaProIleGluProThrProAlaSer	800
Db	2342	GGCCCCACCCACCACCGAGAGACATCCGGGGCCCCCATTGAGCCACCCCGGCTCT	2401
Qy	801	GluAlaThrGlyAlaProThrProProProAlaProProSerProSerAlaProProPro	820
Db	2402	GAAGCCACCGAGCGCCCTAGCGCCCCACACAGCACCCCATCGCTCTGCACCTCTCTCT	2461
Qy	821	ValValProLysGluGluLysGluGluGluThrAlaAlaProProValGluGluGly	840
Db	2462	GTGTGTCCTCCAGGAGGAGAGAGGAGGAGACCGCAGCGCCCCCAGTGGAGGAGGGG	2521
Qy	841	GluGluGlnLysProProAlaAlaGluGluLeuAlaValAspThrGlyLysAlaGluGlu	860
Db	2522	GAGGAGCAGAAGCCCCCGCGCTGAGGAGCTGGCAGTGGACACAGAGGAGGCGGAG	2581
Qy	861	ProValLysSerGluCysThrGluGluAlaGluGluGlyProAlaLysGlyLysAspAla	880
Db	2582	CCCGTCAAGAGCGAGTGCACGGAGGAAGCCGAGAGGGGCGCGCAAGGCAAGGACGCG	2641
Qy	881	GluAlaAlaGluAlaThrAlaGluGlyAlaLeuLysAlaGluLysGlyGlySer	900
Db	2642	GAGCCCGCTGAGGCCACCGCGCGAGGGGCGCTCAAGGCACAGAAAGGAGGCGCGGAGC	2701
Qy	901	GlyArgAlaThrAlaLysSerSerGlyAlaProGlnAspSerAspSerSerAlaThr	920
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Qy	921	CysSerAlaAspGluValAspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerPro	940
Db	2762	TGCAGTGCAGACGAGGTGGATGAGCGCCGAGCGGCGACAAAGACCGCTGCTGCCCA	2821
Qy	941	ArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSerProGlnLysPro	960
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Db	3002	CCACCGAAAACCTGACCGCGAGGCGCGCCCTCAGCAGCGCTGCGACGAGCCCCCGG	3061

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Db	3242	GGTCAACCATGTCCTCGCTGGCGCTCCATGACACTGCCCGGCGCGCTCTCTGCGCGCGCCACCC	3301															
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Db	3302	ACCATCTCCAAACCGGCTCCCTTCATCTCTCTGCCAAAGCACCCACGCTCCTCGAGAGG	3361															
Qy	1121	Gln	Ile	Gly	Ala	Ile	Ser	Gln	Gly	Met	Ser	Val	Gln	Leu	His	Val	Pro	Tyr
Db	3362	CAATAGCTGCGCATCTCCCAAGGATGTCCGTCCAGTCCACGTCCCGTACTCAGAGCAT	3421															
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RESULT 3
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; Sequence 653 Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 653
; LENGTH: 8667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-653

Alignment Scores:
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Score: 13145.00 Matches: 2509
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Db 4435 CTTGGCCCCCGGCGCGCTCAAGAGGGCTTCATCACGAGGGCACCCCGCTCAAGTACGA 4494
Qy 1460 pThrGlyAlaSerThrThrGlySerLysLysHisAspValArgSerLeuIleGlySerPr 1480
Db 4495 CACCGGGCGTCCACCATCTGGCTCCAAAAGACAGAGTACGCTCCCTCATCGGACGCC 4554
Qy 1480 oGlyArgThrPheProProValHisProLeuAspValMetAlaAspAlaAlaLeuGl 1500
Db 4555 CGGCCGGACGTTCCCAACCGCTGCACCGCTGGATGTGATGGCGACGCGCCGGCAGCTGGA 4614
Qy 1500 uArgAlaCysTyrGluGluSerLeuLysSerArgProGlyThrAlaSerSerSerGlyGl 1520
Db 4615 AGTGTCTCTACGAGGAGGCTGAAGAGCGCGCCAGGAGACCGCCAGAGCTCGGGGG 4674
Qy 1520 ySerIleAlaArgGlyAlaProValIleValProGluLeuGlyLysProArgGlnSerPr 1540
Db 4675 CTCCATTCGGCGGGCGCCCGCTCATTTGTCTCTGAGCTGGGCAAGCGCGGAGAGCCC 4734
Qy 1540 oLeuThrTyrGluAspHisGlyAlaProPheAlaGlyHisLeuProArgGlySerProVa 1560
Db 4735 CCTAACCTATGAGGACACAGGGGACCCCTTTGCGGGCACCTCCACAGAGGTTCCGCCGT 4794
Qy 1560 lThrMetArgGluProThrProArgLeuGlnGlySerLeuSerSerSerLysAlaSe 1580
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Qy 1580 rGlnAspArgLysLeuThrSerThrProArgGluIleAlaLysSerProHisSerThrVa 1600
Db 4855 CCAGGACCGAAGAGTGAAGTGCAGCGCTCTGTGATGTCGCAAGTCCCCCGGAGACCGCT 4914
Qy 1600 lProGluHisHisProHisProIleSerProTyrGluHisLeuLeuArgGlyValSerGl 1620
Db 4915 GCGCGAGCACCCACACCCCATCTCGCCCTATGAGCACCTGCTTTCGGGGCGGTGAGTGG 4974

QY 1620 yValAspLeuTyrArgSerHisIleProLeuAlaPheAspProThrSerIleProArgG1 1640
DB 4975 CGTGGACCTGTATCGAGCAGCATCCCTCGCTGGCTTCGACCCACCTCATACCCCGCG 5034
QY 1640 yIleProLeuAspAlaAlaAlaTyrTyrLeuProArgHisLeuAlaProAsnProTh 1660
DB 5035 CATCCCTCTGGACGACGCTGCCTACTACCTGCGCCGACACCTGGCCCCCAACCCAC 5094
QY 1660 rTyrProHisLeuTyrProProTyrIleuIleArgGlyTyrProAspThrAlaAlaLeuG1 1680
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QY 1680 uAsnArgGlnThrIleIleAsnAspTyrIleThrSerGlnGlnMetHisHisAsnThrAl 1700
DB 5155 GAACCGGACAGCATCATCATGACTACATCACTCGAGCAGATGCACCAACACCGCGC 5214
QY 1700 aThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeuSerProArgGluSerSerLe 1720
DB 5215 CACCGCATGGCCAGCGAGCTGATATGCTGAGGGGCTCTCGCCCGCGAGTCTCGCT 5274
QY 1720 uAlaLeuAsnTyrAlaAlaGlyProArgGlyIleIleAspLeuSerGlnValProHisLe 1740
DB 5275 GGCACCTCAACTACGCTGCGGGTCCCGAGGCATCATCGACCTGTCCAAAGTGCACACT 5334
QY 1740 uProValLeuValProProThrProGlyThrProAlaThrAlaMetAspArgLeuAlaTy 1760
DB 5335 GCCTGTGCTGTCGCCCCGACACAGCAGCCACCCGACCATCGCATCGAGCGCTTCCTTA 5394
QY 1760 rLeuProThrAlaProGlnProPheSerSerArgHisSerSerSerProLeuSerProGl 1780
DB 5395 CTTCCCAACCGCGCCAGCCCTTCAGACGCGCCACAGCAGCTCCCACTCTCCCGAGG 5454
QY 1780 yGlyProThrHisLeuThrIleProThrThrThrThrSerSerSerGluArgGluArgAspAr 1800
DB 5455 AGTGTCAACACACTTGACAAACCAACCAACCCAGCTCTCGTCCGAGCGGAGGAGACCG 5514
QY 1800 sAspArgGluArgAspArgGluArgGluLysSerIleLeuThrSerThrThrTh 1820
DB 5515 GGATCAGAGCGGAGCGGGATCGGAGCGGGGAAAGTCCATCTCAGCTCCACACAGAC 5574
QY 1820 rValGluHisAlaProIleTrpArgProGlyThrGluGlnSerSerGlySerSerGlySe 1840
DB 5575 GGTGGAGCAGCACCCATCTGGAGACTGTGTACAGACGAGCAGCGGCGGAGCGGAG 5634
QY 1840 rSerGlyGlyGlyGlySerSerSerArgProAlaSerHisSerHisAlaHisGlnHi 1860
DB 5635 CAGCGCGGGGGTGGGGGCGAGCAGCGCCCGCTCCCACTCCCATGCCCAACAGCA 5694
QY 1860 sSerProIleSerProArgThrGlnAspAlaLeuGlnGlnArgProSerValLeuHisAs 1880
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QY 1920 oLeuGlyGlyThrLeuAspGlyValTyrProThrLeuMetGluProValLeuLeuProLy 1940
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QY 1940 sGluAlaProArgValAlaArgProGluArgProAlaAspThrGlyHisAlaPheLe 1960
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QY 1960 uAlaLysProProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGl 1980
DB 5995 CGCCAAAGCCCCGCGCTCCGGGGTGGAGCCCGCTCTCTCCCGCAGCAAGGGGCTCGGA 6054

QY 1980 uProArgProLeuValProProValSerGlyHisAlaThrIleAlaAArgThrProAlaTy 2000
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QY 2000 sAsnLeuAlaProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAs 2020
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QY 2020 pProHisArgGluLysThrGlnSerLysProPheSerIleGlnGluLeuGluLysArgSe 2040
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QY 2040 rLeuGlyTyrHisGlySerSerTyrSerProGluGlyValGluProValSerProValSe 2060
DB 6235 TCTGGGTATACCAACGCGCAGCAGCTACAGCCCCGAAGGGGTGGAGCCGCTCAGCCCTGTAG 6294
QY 2060 rSerProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluGluLysAspLysSe 2080
DB 6295 CTCACCCAGTCTGACCCACGACGAAGGGGTCTCCCAAGCACCTTGAAGAGCTCGACAGAG 6354
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DB 6355 CCACCTGGAGGGAGCTCGGCCCCAGCAGCCAGCCCCCGTGAAGCTTGGCGGGGAGGC 6414
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DB 6415 CGCCCACTCCCAACCTGCGCGCTGCTGAGAGCCAGCCCTGCTCAGCCCGCTGCT 6474
QY 2120 uGlnThrAlaProGlyValLysGlyHisGlnArgValValThrLeuAlaGlnHisIleSe 2140
DB 6475 CCAGACCGCCCCCAGGGGTCAAGGTACACAGCGGGTGGTCACTCGCTGGCCAGCACATCAG 6534
QY 2140 rGluValIleThrGlnAspTyrThrArgHisHisProGlnGlnLeuSerAlaProLeuPr 2160
DB 6535 TGAGGTATCATCAGAGACTACACCGGCACCAACAGCAGCTCAGCGCACCCCTGCC 6594
QY 2160 oAlaProLeuTyrSerPheProGlyAlaSerCysProValLeuAspLeuArgArgProPr 2180
DB 6595 CGCCCCCTCTACTCTCTCTGGGCGCAGCTGCCCGCTCTGGACCTCCGCGGCCACC 6654
QY 2180 oSerAspLeuTyrLeuProProProAspHisGlyAlaProAlaArgGlySerProHisSe 2200
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QY 2200 rGluGlyGlyLysArgSerProGluProAsnLysThrSerValLeuGlyGlyGlyGluAs 2220
DB 6715 CGAAGGGGCAAGAGTCTCAGAGCCAAACAGAGCTCGTCTTGGGTGGTGGGA 6774
QY 2220 pGlyIleGluProValSerProGluGlyMetThrGluProGlyHisSerArgSerAl 2240
DB 6775 CGGTATTGAACCTGTGTCCCAACCGGAGGGCATGACGGAGCCAGGGCAGCTCCCGAGTGC 6834
QY 2240 aValTyrProLeuLeuTyrArgAspGlyGluGlnThrGluProSerArgMetGlySerLy 2260
DB 6835 TGTGTACCCGCTGCTGTACCGGATGGGAAACAGACGGAGCCAGCAGATGGGCTCCAA 6894
QY 2260 sSerProGlyAsnThrSerGlnProProAlaPhePheSerLysLeuThrGluSerAsnSe 2280
DB 6895 GTCTCAGGCAACACACGACCGCCGCGCTCTTTCAGCAGCTGACCGAGAGCAACTC 6954
QY 2280 rAlaMetValLysSerLysGlnGluIleAsnLysLysLeuAsnThrHisAsnArgAs 2300
DB 6955 CGCCATGGTCAAGTCCAAAGCAAGAGATCAACAAGAAAGCTCAACACCAACCAACCGAA 7014
QY 2300 nGluProGluTyrAsnIleSerGlnProGlyThrGluIlePheAsnMetProAlaIleTh 2320
DB 7015 TGAGCCTGAATCAATATCAGCAGCTGGAGCGGAGATCTTCAATATGCCCGCCATCAC 7074
QY 2320 rGlyThrGlyLeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMe 2340
DB 7075 CGGACAGACGCTTATGACCTATAGAAGCCAGCGGCTGAGGAACATGCCAGCAACCAAT 7134
QY 2340 tGlyLeuGluAlaIleArgLysAlaLeuMetGlyLysTyrAspGlnTrpGluLys 2360

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Db 7135 GGGGCTGAGGCCATAATTAGAAAGGCACATCGGTAAATATACACAGTGGGAAGAGTC 7194
Qy rProProLeuSerAlaAlaSerAlaPheAsnProLeuAsnAlaSerAlaSerLeuProAlaA1 2380
Db 7195 CCGCGGCTCAGCGCCCAATGCTTTTAACTCTGATGCCAGTGCAGCCCTGCCCGTGC 7254
Qy 2380 aMetProileThrAlaAlaSerGlyArgSerAspHisThrLeuThrSerProGlyGlyG1 2400
Db 7255 TATGCCATAACCGCTGCTGACGAGCGAGTGACACACACTCACTCGCCAGGTGGCGG 7314
Qy 2400 yGlyAlaAlaValSerGlyArgProSerSerArgAlaAlaValSerProAlaProG1 2420
Db 7315 CGGGAAGGCCAAGGCTCTGCGACACCGAGCGGAGCCGAAAGCCAAAGTCCCGGCCCGGG 7374
Qy 2420 yLeuAlaSerGlyAspArgProProSerValSerSerValHisSerGluGlyAspCysAs 2440
Db 7375 CTTGGCATCTGGGACCGCGCCACCTCTGCTCTCAGTGACCTCGGAGGAGACTGCAA 7434
Qy 2440 nArgArgThrProLeuThrAsnArgValTrpGluAspArgProSerSerAlaGlySerTh 2460
Db 7435 CCGCGGACGCGCTCACCAACCGCGTGTGGAGGACAGGCCCTCGTCCGAGGTTCCAC 7494
Qy 2460 rProPheProTrpAsnProLeuThrMetArgLeuGlnAlaGlyValMetAlaSerProPr 2480
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Qy 2480 oProProGlyLeuProAlaGlySerGlyProLeuAlaGlyProHisAlaTrpAspG1 2500
Db 7555 CCACCGGGGCTCCCGGGGACGCGGCCCTCGCTGGCCCCCACCACCGCTGGGACGA 7614
Qy 2500 uGluProLysProLeuLeuCysSerGlnTrpGluThrLeuSerAspSerGlu 2517
Db 7615 GGAGCCCAAGCCACTGCTCTGCTGCGAGTACGAGACACTCTCCGACAGCGAG 7666
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RESULT 4

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US-09-819-104A-3
; Sequence 3, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND US$ THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7521)
US-09-819-104A-3
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Pred. No.: 0 Length: 7521
Score: 12978.00 Matches: 2487
Percent Similarity: 98.57% Conservative: 3
Best Local Similarity: 98.46% Mismatches: 9
Query Match: 98.21% Indels: 28
DB: 10 Gaps: 3
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US-09-522-753-5 (1-2517) x US-09-819-104A-3 (1-7521)

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Qy 21 ProHisSerLeuSerTyrProValGlnIleAlaArgThrHisThrAspValGlyLeuLeu 40
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Qy 41 GluTyrGlnHisHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleIleGln 60
Db 121 GAGTACCAGCACCACTCCCGGACTATGCTCTCCACCTGTCCCGCGGCTCCATCATCAG 180
Qy 61 ProGlnArgArgArgProSerLeuLeuSerGluPheGlnProGlyAsnGluArgSerGln 80
Db 181 CCCACGCGGAGGCCCTCCCTGCTGCTGAGTTCAGCCCGGAAATGAACGCTCCAG 240
Qy 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
Db 241 GAGCTCCACCTGGCGGCAGAGTCCCACTCATACCTGCCCGAGCTGGGAAATGACAGATG 300
Qy 101 GluPheIleGluSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
Db 301 GAGTTCAATTGAAGCAAGCGCCCTCGGCTAGAGTGTGCTGACCTGCCCTGCTCGACCG 360
Qy 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
Db 361 TCACCCCTGTGGCCACGGCCAGCTGCGGATCTGAAGACCTCACCAAGGACCGTAGC 420
Qy 141 LeuThrGlyLysLeuGluProValSerProProSerProHisThrAspProGluLeu 160
Db 421 CTGACGGGCAAGTGGAAACCGGTGTCTCCCGCCAGCCCGCCGACACTGACCTGAGCTG 480
Qy 161 GluLeuValProProArgLeuSerLysGluLeuIleGlnAsnMetAspArgValAsp 180
Db 481 GAGCTGTGTCGGCCACCGCTGTCCAAGGAGGAGTGTATCCAGAACATGGACCGCGTGAC 540
Qy 181 ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGlnLeu 200
Db 541 CGAGAGTACCATGGTAGAGCAGCAGATCTTAAGCTGAAGAGAGACGACACAGCTG 600
Qy 201 GluGluGluAlaLysProProGluProGluLysProValSerProProProIleGlu 220
Db 601 GAGGAGGAGGCTGCCAAGCGCCGAGCCTGAGAAGCCCGTGTCCACCGCCCGCCATCGAG 660
Qy 221 SerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysLysAlaGluAla 240
Db 661 TCGAAGCACCAGCGACCTGTGTGCAGATCATCTACGACGAGAACCGGAAGAGGCTGAAGCT 720
Qy 241 AlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGlnPro 260
Db 721 GCACATCGGATTTCTGGNAGSCCTGGGGCCCCAGGTGGAGTGGCGCTGTACACACGCC 780
Qy 261 SerAspThrArgGlnTyrHisGluAsnIleLysIleAsnGlnAlaMetArgLysLysLeu 280
Db 781 TCCGACACCCGCGAGTATCATGAGAACATCAAAATAAACCCAGGCGCATGCGGAAGAGCTA 840
Qy 281 IleLeuTyrPheLysArgAsnHisAlaArgLysGlnTrpLysGlnLysPheCysGln 300
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Qy 301 ArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGluArgIleGluAsnAspPro 320
Db 901 CGCTATGACCAGCTCATGAGGGCTGGGAGAGAGAGTGGAGCGCATGCGGAACAACACCCC 960
Qy 321 ArgArgArgAlaLysGluSerLysValArgGluTyrTyrGluLysGlnPheProGluIle 340
Db 961 CGGCGGCGGCCCAAGGAGAGCAAGTTTCGCGAGTACTACGAGAAGCAGATTTCCCTGAGATC 1020
Qy 341 ArgLysGlnArgGluLeuGlnArgMetGlnSerArgValGlyGlnArgGlySerGly 360
Db 1021 CGCAAGCAGCGGAGCTGCGAGGAGCGCATCGAG ---AGGGTGGGCCCGCGGGCAGTGGG 1077
Qy 361 LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeuSer 380
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Qy 381 GluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeuTyr 400
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Db	1138	GAGCAGGAGACCTGGAGAGCAGATGCGCCAGCTGGCGGTGATCCGCCCATGCTGTAC	1197	Db	2167	ACTGTCAACAAACAGCTCAGACACCGAGAGCATCCCTCTCTCCTCAGACTGAGCGCCGCAAG	2226
Qy	401	AspAlaAspGlnArgIleIysPheIleAsnMetAsnGlyLeuMetAlaAspProMet	420	Qy	761	AspThrGlyGlnAsnGlyProIysProAlaThrLeuGlyAlaAspGlyProProPro	780
Db	1198	GAGCGTGACAGCAGCGCATCAAGTTCATCAATGAAAGCGGCTTATGGCCGACCCCATG	1257	Db	2227	GACACAGGAGAGATGGGCCCAAGCCCGCCAGCCCTCTGGCGCCCGACGGGCCACCCCA	2286
Qy	421	LysValTyrIysAspArgGlnValMetAsnMetTrpSerGluGlnGluIysGluThrPhe	440	Qy	781	GlyProProThrProPro-ArgArgThrSerAlaProIleGluProThrProAlaSe	800
Db	1258	AAGGTGTACAAAGACCGCCAGGTCTATGAACATGTGGAGTGAGCAGAGAGAGACCTTC	1317	Db	2287	GGGCCACCCACCCACCCAGCAGGAGCATCCCGGCC-CCCACTGAGTCCACCCCGGCGCTC	2345
Qy	441	ArgGluIysPheMetGlnHisProIysAsnPheGlyLeuIleAlaSerPheLeuGluArg	460	Qy	800	rGluAlaThrGlyAlaProThrProProAlaProProSerProSerAlaProProPr	820
Db	1318	CGGAGAGTTCATGACGATCCCAAGAACTTTGGCTCATGCGCATTCCTGGAGAGG	1377	Db	2346	TGAAGCACCTTAGCCCTAGCCCGCCACAGCACCCCACTTCCCTCTCTCCTCTCTCC	2405
Qy	461	LysThrValAlaGluCysValLeuTyrTyrLeuThrIysIysAsnGluAsnTyrIys	480	Qy	820	oValValProIysGluGluIysGluGluThrAlaAlaAlaProProValGluGluGlu	840
Db	1378	AAGACGTGGCTGAGTGGCTCTTATTACTGACTAAGNAGAAATGAGAACTATAAG	1437	Db	2406	TGTGGTCCCAAG	2465
Qy	481	SerLeuValArgArgSerTyrArgArgGlyIysSerGlnGlnGlnGlnGlnGlnGln	500	Qy	840	yGluGluGlnIysProProAlaAlaGluGluLeuAlaValAspThrGlyIysAlaGluGlu	860
Db	1438	AGCTGTGTGAGAGGAGCTATCGCGCGCGCGCAAGAGCCAGCAGCAACAACAGCAGAG	1497	Db	2466	GGAGGAGCAGAAGCCCGCGCGCTGAGGAGCTGGCAGTGGCAGACAGGAGAGCGCGAG	2525
Qy	501	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	520	Qy	860	uProValIysSerGluCysThrGluAlaGluGluGluGluGluGluGluGluGluGluGlu	880
Db	1498	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1557	Db	2526	GCCCGTCAAGAGCGAGTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2585
Qy	521	AspGluIysGluIysGluIysGluAlaGluIysGluGluIysProGluValGluAsn	540	Qy	880	aGluAlaAlaGluAlaThrAlaGluGlyAlaLeuIysAlaGluIysGluGlyGlySe	900
Db	1558	GATGAG	1617	Db	2586	GGAGGCCCTGAGGCCACCGCGGAGAGGGCGCTCAAGCAGAGAGAGAGAGAGAGAGAG	2645
Qy	541	AspIysGluAspLeuLeuIysGluIysThrAspAspThrSerGlyIysAspAspGlu	560	Qy	900	rGlyArgAlaThrThrAlaIysSerSerGlyAlaProGlnAspSerAspSerAlaTh	920
Db	1618	GACAAGGAGACCTCCTCAAGGAGAGACAGACACACCTCAGGGAGAGACAGCAGAG	1677	Db	2646	CGGCAGGCGCCACCAAGAGAGAGCTCGGGCGCCCGCCAGGAGAGAGAGAGAGAGAG	2705
Qy	561	LysGluAlaValAlaSerLysGlyArgGlyThrAlaAsnSerGlnGlyArgGlyGly	580	Qy	920	rCysSerAlaAspGluValAspGluAlaGluGlyIysAspIysAsnArgLeuLeuSerPr	940
Db	1678	AAGGAGGCTGTGGCTTCCAAAGGCGCGCAAACTGCCAACAGCCAGGAGAGAGAG	1737	Db	2706	CTGCAGTGAGACAGAGTGATGAGCGCGAGGGCGCGCAGCAAGAACCGGCTGTGTCCC	2765
Qy	581	ArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluGluAlaIleThrProGlnGln	600	Qy	940	oArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSerProGlnIysPr	960
Db	1738	CGCATCACCCGCTCAATGGTAAATGAGGCCAACAGCAGGAGGAGGCGCATCACCCCG	1797	Db	2766	AAGGCCAGCCTCTCTCACCCGACTGGGAGACCCCGGGCCAAATGCTCACCCCAAGAGCC	2825
Qy	601	SerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArgTrpThrGluGluMet	620	Qy	960	oLeuAspLeuIysGlnLeuIysGlnArgAlaAlaIleProProIleGlnValThrLy	980
Db	1798	AGCGCGAGCTGGCTTCCATGAGCTGAATGAGAGTCTCTGCTGACAGAGAGAAATG	1857	Db	2826	ACTGGACCTGAGAGAGCTGAGCAGGAGCGGCTGCCATCCCCCCTCCAGGTCAACAA	2885
Qy	621	GluThrAlaIysLysGlyLeuLeuGluHisGlyArgAsnTrpSerAlaIleAlaArgMet	640	Qy	980	sValHisGluProProArgGluAspAlaAlaProThrIysProAlaProProAlaProPr	1000
Db	1858	GAACACAGCAAGAAAGGTCTCTGGAAACACGCGCGCAACTGTCGCGCATCGCCGGATG	1917	Db	2886	AGTCCATGAGCCCCCGCGGAGAGCGAGCTCCACCAAGCCAGCTCCCGCCAGCCCAAC	2945
Qy	641	ValGlySerLysThrValSerGlnCysIysAsnPheTyrPheAsnTyrLysIysArgGln	660	Qy	1000	oProProGlnAsnLeuGlnProGluSerAspAlaProGlnGlnProGlySerSerProAr	1020
Db	1918	GTGGGCTCCAGACTGTGTGCGAGGTGAAGAACTTCTACTTCAACTCAAGAGAGGCGAG	1977	Db	2946	GCCACGCAAAACCTGACGCGGAGAGCGCCCTCAGCAGCTTCAGCAGCTGGCAGAGCCCG	3005
Qy	661	AsnLeuAspGluIleLeuGlnGlnHisIlysLeuIysMetGluIysGluArgAsnAlaArg	680	Qy	1020	gGlyIysSerArgSerProAlaProProAlaAspIysGlu-----	1033
Db	1978	AACCTCGATGAGATCTTGACGAGCAGCAACAGCTGAAGATGGAGAGAGAGAGAGAG	2037	Db	3006	GGGACAG	3065
Qy	681	ArgLysLysLysAlaProAlaAlaSerGluGluAlaAlaPheProProValVal	700	Qy	1034	----AlaPheAlaAlaGluAlaGlnIysLeuProGlyAspProProCysTrpThrSerG	1052
Db	2038	AGGAG	2097	Db	3066	CCGAGCCTTCGACGCGAGGCGCCAGAGCTGCTGGGGAGCCCGCTTGTGGACTTCCGG	3125
Qy	701	GluAspGluGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGluGlu	720	Qy	1052	yLeuProPheProValProProArgGluValIleIysAlaSerProHisAlaProAspPr	1072
Db	2098	GAGGATGAGGAGATGAGGCGTGGCGGTGAGGAAATGAGAGAGAGATGTTGGAGGAG	2157	Db	3126	CCTGCCCTTCCCGTGGCGCCCGCTGAGGTGATCAAGGCTCCCGCATGCGCGAGCC	3185
Qy	721	AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla	740	Qy	1072	oSerAlaPheSerTyrAlaProProGlyHisProLeuProLeuGlyLeuHisAspThrAl	1092
Db	2158	GCTGAA-----GCC	2166	Db	3186	CTCAGCCTTCTCTACGCTCCACTGTGTCAACCCCACTGCCCTGGGCTCCATGACACTGC	3245
Qy	741	ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaIys	760	Qy	1092	aArgProValLeuProArgProProThrIleSerAsnProProProLeuIleSerSerAl	1112
Db				Db	3246	CCGCGCGCTCTGCGCGCGCCACCCACCATCTCCAAACCCCGCTTCCCTCATCTCTCTGC	3305

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1132 nLeuHisValProTyrSerGluHisAlaLysAlaProValGlyProValThrMetGlyLe 1152 DB
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1366 GCTCCACGTCCTGACAGAGCAATAGGTGCCATCTCCCAAGGAATGTGGTCCA 3365 DB
1366 GCTCCACGTCCTGACAGAGCAATAGGTGCCATCTCCCAAGGAATGTGGTCCA 3365 DB
1152 uProLeuProMetAspProLysLysLeuAlaProPheSerGlyValLysGlnGluLe 1172 QY
1172 uProLeuProMetAspProLysLysLeuAlaProPheSerGlyValLysGlnGluLe 1172 QY
13426 GCGCCCTGCCATGACCCCAAGAGCTGGCACCTTTCAGCGAGTGAAGCAGAGCAGCT 3485 DB
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13486 GTCCCCACGGGGCCAGGCTGGGCCACCGGAGAGCTGGGGTGCACAGCCAGGAGGC 3545 DB
1192 aSerValLeuArgGlyThrAlaLeuGlySerValProGlyGlySerIleThrLysGlyI 1212 QY
1212 aSerValLeuArgGlyThrAlaLeuGlySerValProGlyGlySerIleThrLysGlyI 1212 QY
13546 GTCCGTGCTGAGAGGAGCAGCTCTGGGCTCAGTTCCGGGGGGAAGCATCAACAAAGCAT 3605 DB
1212 eProSerThrArgValProSerAspSerAlaIleThrTyrArgGlySerIleThrHisGI 1232 QY
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13606 TCCAGCACAGGCTGCTCGGACAGGCGCATCACATACCGCGGCTCCATCACCACGG 3665 DB
1232 YThrProAlaAspValLeuTyrLysGlyThrIleThrArgIleIleGlyGluAspSerPr 1252 QY
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13666 CACGCCAGCTGACCTCTGTACAAAGGACCATCACAGGATCATCCGGGAGGACAGCCC 3725 DB
1252 oSerArgLeuAspArgGlyArgGluAspSerLeuProLysGlyHisValIleTyrGluGI 1272 QY
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13726 GAGTCGCTTGGACCGCGCGGGAGGACAGCTCTCCCAAGGGCCACGTCTACTACGAAGG 3785 DB
1272 YLysLysGlyHisValLeuSerTyrGluGlyGlyMetSerValThrGlnCysSerLysGI 1292 QY
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1372 gArgGluAlaLysLeuLysArgGluGlyThrProProProProProSerArgAs 1392 QY
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|||||
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5586 GCAGAGACCCAGTGTCTTACAAACACAGCAATGAAGGGTATCATCACCGCTGTGGAGCC 5645
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1892 oSerLysProThrValLeuArgSerThrSerSerProValArgProAlaAlaTh 1912
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5826 AGCAGACACCGGCATGCCCTCTCCGCCAAGCCGCCAGCCCGCTCCGGGTGGAGCCCGC 5885
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RESULT 5

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; Sequence 1, Application US/09819104A

; Publication No. US20030027137A1

; GENERAL INFORMATION:

; APPLICANT: Chen, J. Don

; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES

; TITLE OF INVENTION: AND USES THEREFOR

; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(7677)
US-09-819-104A-1

Alignment Scores:

Pred. No.: 0 Length: 8686
Score: 12378.00 Matches: 2487
Percent Similarity: 98.57% Conservative: 3
Best Local Similarity: 98.46% Mismatches: 9
Query Match: 98.21% Indels: 28
DB: 10 Gaps: 3

US-09-522-753-5 (1-2517) x US-09-819-104A-1 (1-8686)

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DB 217 CCCCACAGCCTTTCCTACCCAGTGCAGATGCCCGGACGACACGAGCGTCCGGCTCCTG 276
QY 41 GluTyrGlnHisHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleLeuGln 60
DB 277 GAGTACAGCAGCACCCTCCCGCAGTATGCCCTCCACCTGTGCGCCCGCTCCATCATCCAG 336
QY 61 ProGluArgArgProSerLeuLeuSerGluPheGlnProGlyAenGluArgSerGln 80
DB 337 CCCACGGCGGAGGCGCTCCCTGCTGTCTGAGTTCAGGCCCGGGAATGAACGGTCCCAG 396
QY 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
DB 397 GAGCTCCACTGCGGCAGAGTCCCACTATACCTGCCAGCTGGGGAAGTCAAGATG 456
QY 101 GluPheIleGluSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
DB 457 GAGTTCATTGAAGCAAGCGCCCTCGCTAGAGCTGCTGACCCCTGCTGCGACCG 516
QY 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
DB 517 TCACCCCTGCTGCGCCAGCGGCCAGCTGCGGGATCTGAAGACCTCACCAGGACCGTAGC 576
QY 141 LeuThrGlyLysLeuGluProValSerProProSerProHisThrAspProGluLeu 160
DB 577 CTGACGGGCAAGCTGGAAACGGGTGTCTCCCCCAGCCCCCGCACACTGACCTCGAGCTG 636
QY 161 GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAenMetAspArgValAsp 180
DB 637 GAGCTGTGCGCCAGCGCTGTCCAGGAGGAGCTGATCCAGAACTATGAGACCGCTGGAC 696
QY 181 ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnLeu 200
DB 697 CGAGAGATCACCTAGTAGAGCAGCAGATCTCTAAGCTGAAGAGAGAGCAGCAACAGCTG 756
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DB 757 GAGGAGGAGGCTGCCAAGCGCCCGGAGCTGAGAGCCCGTGTACCGCGCCCATCGAG 816
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DB 877 GCACATCGGATCTCGAAGCGCTGGGGCCCGCAGGTGGAGTGGCGCTGTACACACCGCCC 936
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DB 937 TCCGACACCGCGCAGTATCATGAGAACATCAAAATAAACCCAGCGCATCGGAAGAGCTA 996
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QY 341 ArgLysGlnArgGlnLeuGlnArgMetGlnSerArgValGlyGlnArgGlySerGly 360
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DB 1714 GATGAAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1773
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DB 1774 GACNAGAGAGCTCTCTCAAGGAGAGACAGACACACCTCAGGGAGGAGCAACAGCAG 1833
QY 561 LysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSerGlnGlyArgLysGly 580
DB 1834 AAGGAGGCTGTGCGCTCCAAAGCGCCCAAACTGCCCAACAGCCAGGAGAGCAAGGC 1893
QY 581 ArgIleThrArgSerMetAlaAenGluAlaAenSerGluGluAlaIleThrProGlnGln 600
DB 1894 CGCATCACCGCTCAATGGCTAATGAGGCCAACAGGAGGAGGAGGAGGAGGAGGAGGAG 1953

QY	601	SerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArgTTPThrGluGluMet	620	QY	960	oLeuAspLeuLysGlnLeuLysGlnArgAlaAlaAlaIleProProIleGlnValThryl	980
Db	1954	AGCGCCGAGCTGGCTCCATGAGCTGAATGAGAGTTCTCGCTGGACAGAGAGAAATG	2013	Db	2982	ACTGGACCTGAAGCACTGAAGCGGAGCGGCTGCCATCCCCCATCCAGGTCAACAA	3041
QY	621	GluThrAlaLysLysGlyLeuLeuGluHISGlyArgAsnTTPSerAlaIleAlaArgMet	640	QY	980	sValHISGluProProArgGluAspAlaAlaProThryLysProAlaProProAlaProPr	1000
Db	2014	GAAACAGCCAGAAAGGTCTCTGGAAACACGCCCACTGGTCCGCCATCCCGGATG	2073	Db	3042	AGTCCATGAGCCCCCGGAGGAGCAGCTCCCAAGCCAGCTCCCCCAGCCCCACC	3101
QY	641	ValGlySerLysThrValSerGlnCysLysAsnPheTyrPheAsnTyrLysLysArgGln	660	QY	1000	oProProGlnAsnLeuGlnProGluSerAspAlaProGlnGlnProGlyLysSerProAr	1020
Db	2074	GTGGGTCCAAAGACTGTGCGAGTGAAGAACTTCTACTCAACTACAAAGAAAGCGAG	2133	Db	3102	GCCACCGCAAAACCTTGACCGGAGAGCGAGCCCCCTCAGAGCTTGGCAGCAGCCCCG	3161
QY	661	AsnLeuAspGluLeuLeuGlnHISLysLeuLysMetGluLysGluArgAsnAlaArg	680	QY	1020	gGlyLysSerArgSerProAlaProProAlaAspLysGlu-----	1033
Db	2134	AACCTCATGAGATCTTGCAGCAGCACACAGCTGAAGATGAGAAGGAGAGGAACGCGGG	2193	Db	3162	GGGCAAGAGCAGGAGCCCCCGCACCAAGAGGAGGAGAGAGCTGTGTCTTCT	3221
QY	681	ArgLysLysLysLysAlaProAlaAlaAlaSerGluAlaAlaPheProValVal	700	QY	1034	----AlaPheAlaAlaGluAlaGlnLysLeuProGlyAspProProCysTTPThrSerGl	1052
Db	2194	AGGAAGAAGAAAGCGCGCGGCGGCGAGGAGGCTGCATTCGCGCCCGTGGTG	2253	Db	3222	CCCAGCCTTCGAGCGGAGGCGCCAGAGTGCCTGGGAGCCCCCTTGTGGACTTCCGG	3281
QY	701	GluAspGluGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGluGlu	720	QY	1052	yLeuProPheProValProProArgGluValIleLysAlaSerProHisAlaProAspPr	1072
Db	2254	GAGATGAGGAGATGGAGGCGCTCGGCGTGAACCGGAATGAGGAGGATGTGGAGGAG	2313	Db	3282	CCTGCCCTTCCCGTGGCGCCGCCACCACTCCAAACCGGCTCCCTCATCTCTCTGC	3341
QY	721	AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla	740	QY	1072	oSerAlaPheSerTyrAlaProProGlyHisProLeuProLeuGlyLeuHisAspThrAl	1092
Db	2314	GCTGAA-----GCC	2322	Db	3342	CTCAGCCTTCTCTACGCTCCACCTGGTCAACCTCCCTGGGCTCCCTGACACTGC	3401
QY	741	ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaAlaLys	760	QY	1092	aArgProValLeuProArgProProThrIleSerAsnProProProLeuIleSerSerAl	1112
Db	2323	ACTGTCAACAACAGCTCAGACACCGAGAGCATCCCTCTCTCCTACTGAGCGCGCAAG	2382	Db	3402	CGGCGCGCTCTGCGCGGCCGCCACCACTCCAAACCGGCTCCCTCATCTCTCTGC	3461
QY	761	AspThrGlyGlnAsnGlyProLysProProAlaThrLeuGlyAlaAspGlyProProPro	780	QY	1112	alyHisProSerValLeuGluArgGlnIleGlyAlaIleSerGlnGlyMetSerValGl	1132
Db	2383	GACACAGGCGAATGGCCCCAGCCCCCAGCACCTCTGGGCGCGAGCGGCCACCCCCA	2442	Db	3462	CAAGCACCCAGCGCTCTCGAGAGGCAAAATAGTGCCTATCTCCCAAGAAATGTCCGTC	3521
QY	781	GlyProProThrProPro-ArgArgThrSerArgAlaProIleGluProThrProLase	800	QY	1132	nLeuHisValProTyrSerGluHisAlaLysAlaProValGlyProValThrMetGlyLe	1152
Db	2443	GGGCGACCCACCCACCAACCGGAGGACATCCCGGCC-CCCACTGAGTCCACCCCGGCTC	2501	Db	3522	GCTCCACGCTCCCGTACTCAGAGCATGCCAAGCGCCCGGTGGGCGCTGTCCACATGGGG	3581
QY	800	rGluAlaThrGlyAlaProThrProProAlaProProSerProSerAlaProProPr	820	QY	1152	uProLeuProMetAspProLysLysLeuAlaProPheSerGlyValLysGlnGluGlnLe	1172
Db	2502	TGAAGCCACCTTAGCCCTTACGCCCCACAGCAGACCCCTTCCTTCCCTCTTCCCTCTCC	2561	Db	3582	GCCTTGCCTTGGACCCCAAAAGCTGGCACTTCCAGCGAGTGAAGAGGAGGAGCT	3641
QY	820	oValValProLysGluLysGluGluThrAlaAlaAlaProValGluGlu	840	QY	1172	uSerProArgGlyGlnAlaGlyProProGluSerLeuGlyValProThrAlaGlnGluAl	1192
Db	2562	TGTGTCTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2621	Db	3642	GTCCCCACCGGCGGAGGCTGGGCCACCGGAGAGCTGGGGGTGCCACAGGCCAGGAGG	3701
QY	840	yGluGluGlnLysProProAlaAlaGluGluLeuAlaValAspThrGlyLysAlaGluGl	860	QY	1192	aSerValLeuArgGlyThrAlaLeuGlySerValProGlyGlySerIleThrLysGlyLl	1212
Db	2622	GGAGGAGCAGAGCCCGCGGCTGAGAGCTGAGAGCTGAGCAGCAGGAGGAGGAGGAG	2681	Db	3702	GTCCGTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3761
QY	860	uProValLysSerGluCysThrGluGluAlaGluGluProAlaLysGlyLysAspAl	880	QY	1212	eProSerThrArgValProSerAspSerAlaIleThrTyrArgGlySerIleThrHisGl	1232
Db	2682	GCCCGTCAAGAGCGAGTGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2741	Db	3762	TCCAGCACACAGGCTGCCCTCGACAGCGCCATCATACCGCGGTCTCATCACCACCG	3821
QY	880	aGluAlaAlaGluAlaThrAlaGluGlyAlaLeuLysAlaGluLysGlyGlyLys	900	QY	1232	yThrProAlaAspValLeuTyrLysGlyThrIleThrArgIleIleGlyGluAspSerPr	1252
Db	2742	GGAGGCGCTGAGGCCACCGCGAGAGGCGCTCAAGGCGAGCAGCAGGAGGAGGAGG	2801	Db	3822	CAGCGAGCTGAGCGTCTGTACAGGCGCACCATCACCAGCATCATCGGCGAGGAGG	3881
QY	900	rGlyArgAlaThrAlaLysSerSerGlyAlaProGlnAspSerAspSerAlaTh	920	QY	1252	oSerArgLeuAspArgGlyArgGluAspSerLeuProLysGlyHisValIleTyrGluGl	1272
Db	2802	CGGAGGCGCACACAGCCAGAGAGCTCGGCGCCCCCGGAGGAGGAGGAGGAGGAG	2861	Db	3882	GAGTCCGTGGAACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3941
QY	920	rCysSerAlaAspGluValAspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerPr	940	QY	1272	yLysLysGlyHisValLeuSerTyrGluGlyGlyMetSerValThrGlnCysSerLysGl	1292
Db	2862	CTCAGTGCAGACGAGTGGATGAGCGGCGCGCAGAGAACCGGCTCTCTCTCCCC	2921	Db	3942	CAAGAGGCGGCGCATCTGTGCTTATGAGGCTGCACTGTGTGACCCAGTGTCTCAAG	4001
QY	940	oArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSerProGluLysPr	960	QY	1292	uAspGlyArgSerSerSerGlyProProHisGluThrAlaAlaProLysArgThrTyrAs	1312
Db	2922	AGGCGCCAGGCTCTCTACCCCGACTGGCGACCCCGCGGCGCAATGCTCTACCCAGAG	2981	Db	4002	GGAGCGCAGAGCAGCTCAGAGCCCCCATGAGAGCGGCGGCGGCGGCGGCGGCGG	4061
QY	960	oArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSerProGluLysPr	980	QY	1312	pMetMetGluGlyArgValGlyArgAlaIleSerSerAlaSerIleGluGlyLeuMetGl	1332

4062	Db		CATGATGAGGGCGCGTGGGCAGAGCCATCTCTCTCAGCCAGCATCGAAGGTCTCATGGG	4121
1332	Qy	YrGAlaIaIleProGluAargHisSerProHisHisLeuLysGluGlnHisHisIleAr		1352
4122	Db	CCGTGCCATCCCGCGGAGGAGACACAGCCCCCACCACCTCAAGAGCAGCACACATCCG		4181
1352	Qy	gGlySerIleThrGlnGlyIleProAArgSerTyrValGluAaGlnGluAspTyrLeuAr		1372
4182	Db	CGGGTCCATCACACAAAGGATCCCTCGGTCTCTACGTGGAGGCACAGGAGACTACCTGGC		4241
1372	Qy	gArgGluAlaLysLeuLysArgGluGlyIThrProProProProProProSerArgAs		1392
4242	Db	TCGGGAGGCCAAGCTCTCTAAAGCGGAGGAGCAGCCCTCCGCCCCACCAGCCCTCAGGGGA		4301
1392	Qy	pLeuThrGluAlaTyrLysThrGlnAlaLeuGlyProLeuLysLeuLysProAlaHisG1		1412
4302	Db	CCTGACCTGAGGCCCTACAGACGACAGGCCCTGGGGCCCCCTGAGCTGAAGCGGCGCCATGA		4361
1412	Qy	uGlyLeuValAlaThrValLysGluAlaGlyAArgSerIleHisGluIleProArgGluG1		1432
4362	Db	GGGCCTGGTGGCCACGCTGAAGGAGGCGGCGCTCCATCATGAGATCCCGCGCGAGGA		4421
1432	Qy	uLeuAArgHisThrProGluLeuProLeuAlaProAArgProLeuLysGluGlySerIleTh		1452
4422	Db	GCTCGCGCACACGCGCCGAGCTGCCCTCGGCCCGCGCGCTCAAGGAGGGCTCCATCAC		4481
1452	Qy	rGlnGlyThrProLeuLysTyrAapThrGlyAlaSerThrThrGlySerLysLysHisAs		1472
4482	Db	GCAGGGCACCCCGCTCAAGTACACACCGGGCGGTCCACCATGGCTCCAAAAGACACGA		4541
1472	Qy	pValAArgSerLeuIleGlySerProGlyAArgThrPheProProValHisProLeuAspVa		1492
4542	Db	CGTACGCTCCCTCATCGGCAGCCCGCGCGGACGTTCCACCCCGTGACACCGCTGGATGT		4601
1492	Qy	lMetAlaAspAlaAargAlaLeuGluAArgAlaCysTyrGluGluSerIleuLysSerArgPr		1512
4602	Db	GATGGCGCAGCCCGCGCACTTGGAAACGTGCTGCTAGCAGGAGAGCCTGAAGAGCGCGCC		4661
1512	Qy	oGlyThrAlaSerSerGlyGlySerIleAlaAargGlyValaProValIleValProG1		1532
4662	Db	AGGACCGCCAGCAGCTCGGGGGCTCCATTGGCGCGGGCGCCCGGTCAATTGTGCTGA		4721
1532	Qy	uLeuGlyLysProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaG1		1552
4722	Db	GCTGGGTAAAGCGCGGAGAGCCCTCTGACCTATGAGGACCAACGGGGCACCCCTTGCCGG		4781
1552	Qy	yHisLeuProAArgGlySerProValThrMetArgGluProThrProArgLeuGlnGluG1		1572
4782	Db	CCACCTCCACAGGTTCCGCGGTGACCATCGGGAGCCCAACGCGCGCTCGAGGAGGG		4841
1572	Qy	ySerLeuSerSerSerLysAlaSerGlnAspArgLysLeuThrSerThrProArgGluI1		1592
4842	Db	CAGCCTTTGTCACAGCAAGGCATCCCAAGACCCGAAGCTACGCTGACGCTCGTGAGAT		4901
1592	Qy	eAlaLysSerProHisSerThrValProGluHisHisProHisProIleSerProTyrG1		1612
4902	Db	CGCCAACTCCCGCAGACACCGTGCCTGGAGCACCAACCCCATCTCGGCCCTATGA		4961
1612	Qy	uHisLeuLeuAArgGlyValSerGlyValAspLeuTyrArgSerHisIleProLeuAlaph		1632
4962	Db	GCACCTGCTTCGGGCGGTGAGTGGCGGTGGACCTGTATCGCAGGCCACATCCCCCTGGCCTT		5021
1632	Qy	eAspProThrSerIleProArgGlyIleProLeuAspAlaAlaAlaTyrTyrLeuPr		1652
5022	Db	CGACCCCACTTCCATACCCCGCGCACTCCCTCTGGACGACGCGCTGCCCTACTACTGTC		5081
1652	Qy	oAArgHisLeuAlaProAsnProThrTyrProHisLeuTyrProProTyrLeuIleAArgG1		1672
5082	Db	CCGACACTGGCCCCCAACCCCACTACCCGACCTGTACCCACCTTACCTCATTCGCGGG		5141
1672	Qy	yTyrProAspThrAlaAlaLeuGluAAsnAArgGlnThrIleIleAsnAspTyrIleThrSe		1692

5142	Db	CTATCCCGCACACGGCGGGCGCTGGAGAACCGCGCAGACCATCATCAATGACTACATCACCTC	5201
1692	Qy	rGlnGlnMetHisEAsnThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArgG1	1712
5202	Db	GCAGCAGATGCACCAACACACGGCCACCGCATGGCCACGAGGCTGATATGCTGAGGGG	5261
1712	Qy	YLeuSerProArgGluSerSerLeuAlaLeuAenTyrAlaAlaGlyProArgGlyLeI1	1732
5262	Db	CCTCTCGCCCGGAGTCTCTCGCTGGCAGCTCAACTAGCTCGCGGTCCCGAGGCATCAT	5321
1732	Qy	eAspLeuSerGlnValProHisLeuProValLeuValProProThrProGlyThrProAl	1752
5322	Db	CGACCTGTCCCAAGTGCACACCTCGCTGTGCTGGTCCGCCACACGACCGACCCCGCAGC	5381
1752	Qy	aThrAlaMetAspArgLeuAlaTyrLeuProThrAlaProGlnProPheSerSerArgHi	1772
5382	Db	CACCGCATGGACGGCTTGCTTACCTCCCAACCGCGCCCGCCAGCCCTTCAGCAGCGCCA	5441
1772	Qy	sSerSerSerProLeuSerProGlyGlyProThrHisLeuThrLysProThrThrThrSe	1792
5442	Db	CAGCAGCTCCCACTCTCCCGAGAGGTCCAACACACTTGACAAAACCAACCAACCGACGTC	5501
1792	Qy	rSerSerGluArgGluArgAspArgAspArgGluArgAspArgAspArgGluArgGluY	1812
5502	Db	CTCGTCCGACGGGAGCGACACCGGATCGAGAGCGGACCGGGATCGGGAGCGGGAAAA	5561
1812	Qy	sSerIleLeuThrSerThrThrValGluHisAlaProIleTrrArgProGlyThrGl	1832
5562	Db	GTCCATCTCTACGTCCACACGCGGTGGAGCAGCACCCCATCTGGNGACCTGGGTACAGA	5621
1832	Qy	uGlnSerSerGlySerSerGlySerGlyGlyGlyGlyGlySerSerSerArgProAl	1852
5622	Db	GCAGACGACGGCAGCAGCGCAGCAGCGCGGGGTGGGGCAGCAGCAGCGCGCCCGCGC	5681
1852	Qy	aSerHisSerHisAlaHisGlnHisSerProIleSerProArgThrGlnAspAlaLeuGl	1872
5682	Db	CTCCCACTCCCATGCCACACAGCACTCGCCCATCTCCCTCGACCCAGATGCCCTCCA	5741
1872	Qy	nGlnArgProSerValLeuHisAenThrGlyMetLysGlyIleIleThrAlaValGluPr	1892
5742	Db	GCAGAGNCCAGTGTGCTTCACAAACACAGCATGAAGGTATCATCACCCGCTGTGGAGCC	5801
1892	Qy	oSerLysProThrValLeuArgSerThrSerThrSerSerProValArgProAlaAlaTh	1912
5802	Db	CAGCAAGCCACCGTCTCTGAGGTCCACTCCACTCTCTCACCGCTTCGCCCGCAGCTGCCAC	5861
1912	Qy	rPheProProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyrProThrLe	1932
5862	Db	ATTCCCACTGCCACCCACTCGCCACTGGCGCGCACCCCTCGATGGGGTCTTACCCCTACCCT	5921
1932	Qy	uMetGluProValLeuLeuProLysGluAlaProArgValAlaArgProGluArgProAr	1952
5922	Db	CATGGAGCCCGTCTTGCTGCCAAGAGGCCCCCGGGTCCGCCCGCCAGCGGCGCCCGC	5981
1952	Qy	gAlaAspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuGluProAl	1972
5982	Db	AGCAGACACCGGCCATGCCTTCCTGCCAAGCCCCCGCAGCCCGCTCCGGGTGGAGCCCGC	6041
1972	Qy	aSerSerProSerLysGlySerGluProArgProLeuValProProValSerGlyHisAl	1992
6042	Db	CTCTCCCCCAGCAAGGGCTCGAGGCCCCCGGCCCTAGTGCCCTCTGTCTCTGGCCACGC	6101
1992	Qy	aThrIleAlaArgThrProAlaLysAenLeuAlaProHisHisAlaSerProAspProPr	2012
6102	Db	CACCATCGCCCGCACCCCTCGAAGAACCTCGCACCTTCACACGCCAGCCGAGCCCGCC	6161
2012	Qy	oAlaProProAlaSerAlaSerAspProHisArgGluLeuThrGlnSerLysProPheSe	2032
6162	Db	GGCGCCACCTGCCTCGGCCTCGACCCGACCGCACCGGAAAAAGACTCAAAGTAAACCTTTTC	6221
2032	Qy	rIleGlnGluLeuGluLeuArgSerLeuGlyTyrHisGlySerSerTyrSerProGluGl	2052
6222	Db	CATCCAGGAATCGAACTCCGTTCTCTGGGTATCCAGCGCAGCAGCTACAGCCCCGAAGG	6281

Qy	81	GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet	100
Db	397	GAGCTCCACCTCGCGCCAGAGTCCCACTACCTACCTGCGGAGCTGGGGAAGTCAGAGATG	456
Qy	101	GluPheIleGluSerLysArgProArgLeuCluLeuLeuProAspProLeuLeuArgPro	120
Db	457	GAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCTGACCCCTCTGCGACCG	516
Qy	121	SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer	140
Db	517	TCACCCCTGTGGCCACGGGCCAGCTCGGGATCTGAAGACCTCACCAAGGACCGTAGC	576
Qy	141	LeuThrGlyLysLeuGluProValSerProProSerProProHisThrAspProGluLeu	160
Db	577	CTGACGGGCAAGCTGGGAACCGGTGTCTCCCCAGCCGCCCGCACACTGACCTGAGCTG	636
Qy	161	GluLeuValProProArgLeuSerLysGluCluLeuIleGlnAsnMetAspArgValasp	180
Db	637	GAGCTGGTGGCCGACCAGCGCTGTCCAAGAGAGAGTGTATCCAGAACATATGGACCCGCGTGGAC	696
Qy	181	ArgGluIleThrMetValGluGlnGlnIleSerLysLysLeuLysLysGlnGlnLeu	200
Db	697	CGAGAGATCACCATGGTAGACAGCAGATCTCTTAAGCTGAAGAGAGAGCAGCAACAGCTG	756
Qy	201	GluGluAlaAlaLysProProGluProGluLysProValSerProProIleGlu	220
Db	757	GAGGAGGAGGTGCAAGCGCCGCGAGCTGAGAAGCCGCTGTACCCGCCCATCGAG	816
Qy	221	SerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysLysAlaGluAla	240
Db	817	TCGAAGCACCGCACCGCTGGTGCAATCATCTACACAGAGAACCCGGAAGAAGCTGAAGCT	876
Qy	241	AlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGlnPro	260
Db	877	GCACATCGGATCTTGGAAGGCTCGGGCCCCAGCTGGAGCTGCGCGCTGTACACCAAGCCC	936
Qy	261	SerAspThrArgGlnTyrHisGluAsnIleLysIleAsnGlnAlaMetArgLysLysLeu	280
Db	937	TCCGACACCCGGCAGTAGTATCATGAGAACATCAAAATAAACACGAGCGATCGGAAGAAGCTA	996
Qy	281	IleLeuTyrPheLysArgArgAsnHisAlaArgLysGlnTyrLysGlnLysPheCysGln	300
Db	997	ATCTTGACTTCAAGAGGAGGAATCACGCTCGGAACAATGGGAGCAGAAAGTTCTGCGCAG	1056
Qy	301	ArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGluArgIleGluAsnAsnPro	320
Db	1057	CGCTATGACCAAGTTCATGGAGGCTCGGAGAGAGAGGTGGAGCGCATCGAGAACACACCC	1116
Qy	321	ArgArgAlaLysGluSerLysValArgGlnTyrTyrGluLysGlnPheProGluIle	340
Db	1117	CGGCGGCGGCCAAGGAGAGCAAGGTTCCGCGAGTACTACGAGAAGCAGTTCCTCTGAGATC	1176
Qy	341	ArgLysGlnArgGluLeuGlnArgMetClnSerArgValGlyGlnArgGlySerGly	360
Db	1177	CGCAAGCAGCGCGAGCTGACGAGCGCATGCGAG--AGGGTGGGCGCCAGCGGGCGCAGTGGG	1233
Qy	361	LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeuSer	380
Db	1234	CTGTCCATGTCCCGCCGCGCAGCGAGCAGCGAGTGTACAGATCATCGATGGCCTCTCA	1293
Qy	381	GluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeuTyr	400
Db	1294	GAGCAGGAGAACCTGGAGAAGCAGATGCGCCAGCTGGCGGTGATCCCGCCCATGCTGTAC	1353
Qy	401	AspAlaaspGlnArgIleLysPheIleAsnMetAsnGlyLeuMetAlaaspProMet	420
Db	1354	GACGCTGACGACGAGCGCATCAAGTTTCATCAACATGAACCGGCTTATGGCGCGACCCCATG	1413
Qy	421	LysValTyrLysAspArgGlnValMetAsnMetTrpSerGluGlnGluLysGluThrPhe	440
Db	1414	AAGGTGTCAAAAGNCCGCCAGGTCTATGAACATGTGGAGTGTGACGAGGAGGAGGACCTTC	1473
Qy	441	ArgGluLysPheMetGlnHisProLysAsnPheGlyLeuIleAlaSerPheLeuGluArg	460

1474	Db	CGGAGAGGTTTCATGTCAGACATCCCAAGAACTTTGGCTCATCGCATCATTTCTCTGGAGAGG	1533
461	Qy	LyethrValAlaGluCysValLeuTyrTyrLeuThrIlyeIysAenGluAentYrLys	480
1534	Db	AAGACAGTGGCTCAGTGTGCTCTATTACTCTGACTAAGAAGAAATGAGAACTATAAG	1593
481	Qy	SerLeuValArgArgSerTyrArgArgGlyLysSerGlnGlnGlnGlnGlnGln	500
1594	Db	AGCCTGTGTAGACGGAGCTATCGCGCGCGCAAGAGCCAGCAGCAACACAGCAGCAG	1653
501	Qy	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	520
1654	Db	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1713
521	Qy	AspGluLysGluLysGluLysGluAlaGluLysGluGluGluLysProGluValGluAen	540
1714	Db	GATGAGAAGGAGAAGAAAGGAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG	1773
541	Qy	AspLysGluAspLeuLeuLysGluLysThrAspAspThrSerGlyGluAspAenAspGlu	560
1774	Db	GACAAGGAAGACCTCCTCAAGGAGAGACAGACAGCACCTCAGGGGAGGACCAACGAC	1833
561	Qy	LysGluAlaValAlaSerLysGlyArgLysThrAlaAenSerGlnGlyArgArgLysGly	580
1834	Db	AAGGAGGCTGTGGCTTCCAAAGGCGCAAACTGTCCACAGCCAGCGGAAGAGCAAGGC	1893
581	Qy	ArgIleThrArgSerMetAlaAenGluAlaAenSerGluGluAlaIleThrProGlnGln	600
1894	Db	CGCATCACCCGCTCAATGGCTAATGAGGCGCAACAGCGAGGAGGCGCATCACCCCGC	1953
601	Qy	SerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArgTrpThrGluGluMet	620
1954	Db	AGCGCGAGCTGGCTTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAGAGAAATG	2013
621	Qy	GluThrAlaLysLysGlyLeuLeuGluHisGlyArgAsnTrpSerAlaIleAlaArgMet	640
2014	Db	GAACAACGCAAGAAAGGTCTCTCTGGAAACAGCGCGCAACTGTGTGGCCCATCGCCG	2073
641	Qy	ValGlySerLysThrValSerGlnCysLysAenPheTyrPheAsnTrpLysLysArgGln	660
2074	Db	GTGGGCTCCAAAGACTGTGTGCGAGTGTAGAATCTTCTTCAACTACAGAAGAGGCG	2133
661	Qy	AsnLeuAspGluIleLeuGlnGlnHisLysLeuLysMetGluLysGluArgAsnAlaArg	680
2134	Db	AACCTCGATGAGATCTTGACGACGACCAAGCTGAAGATGGAGAAGGAGAGCAACGCG	2193
681	Qy	ArgLysLysLysLysAlaProAlaAlaSerGluGluAlaAlaPheProValVal	700
2194	Db	AGGAAGAAGAAAGCGCGCGCGCGCGCAGCGAGGAGGCTGCATTCCCGCGCTGGTG	2253
701	Qy	GluAspGluMetGluAlaSerGlyValSerGlyAsnGluGluGluMetValGluGlu	720
2254	Db	GAGGATGAGGAGATGAGGCGCTCGGCGGTGACGGAAATGAGAGGAGATGTGTGGAGG	2313
721	Qy	AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla	740
2314	Db	GCTGAA-----GCC	2322
741	Qy	ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaLys	760
2323	Db	ACTGTCAACAACAGCTCAGACACCGAGAGCATCCCTCTCTCTACACTGAGGCGCGCA	2382
761	Qy	AspThrGlyGlnAsnGlyProLysProProAlaThrLeuGluAlaAspGlyProProPro	780
2383	Db	GACACAGGGCAGAAATGGGGCCCAAGCCCCCAGCCACCTGGGGCGCGACGGGCCAC	2442
781	Qy	GlyProProThrProPro-ArgArgThrSerArgAlaProIleGluProThrProAlaSe	800
2443	Db	GGGCCACCCACCCACCGGAGGACATCCGGCC-CCCACTGAGTCCACCCCGGCTTC	2501
800	Qy	rGluAlaThrGlyAlaProThrProProProAlaProProSerProSerAlaProProPr	820

QY 1532 uLeuGlyLysProArgGlnSerProLeuThrThrGluAspHisGlyAlaProPheAlaGI 1552
DB 4722 GCTGGGTAAAGCCGCGCAGAGCCCTTGAATATGAGACACACGGGGCACCCCTTTCGGG 4781
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Score: 10832.50 Matches: 2149
Percent Similarity: 87.94% Conservatives: 90
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DB: 10 Gaps: 33
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; Publication No. US20030027137A1
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; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; FILE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 7386
; TYPE: DNA
; ORGANISM: Mus musculus

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QY	1158	ProLysLysLeuAlaProPheSerGlyValLysGlnGlnLeuSerProArgGlyGln	1177	Db	4432	AGCAGTGTGTGAGGCGGCTCCATCACAGTGGGGCTCCAGTCTGCTGGCTGGAATGGGC	4491
Db	3472	CCTAAGAAGCTG-----	3483	QY	1535	LysProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaGlyHisLeu	1554
QY	1178	AlaGlyProProGluSerLeuGlyValProThrAlaGlnGluAlaSerValLeuArgGly	1197	Db	4492	AAGCCACGCGCAAGCCCACTGACTTACGAAGACCCAGCGGCGACCTTACCAGTCACCTG	4551
Db	3484	-----GGG	3486	QY	1555	ProArgGlySerProValThrMetArgGluProThrProArgLeuGlnGlySerLeu	1574
QY	1198	ThrAlaLeuGlySerValProGlySerIleThrLysGlyIleProSerThrArgVal	1217	Db	4552	CAACGTGGCTCCCTGTGACCAAGGAGGAGCCAGCGCGCTTTCAGAAAGGCGAGCTC	4611
Db	3487	ACAGCACT-GGCTCGCCACCAGTGAAGCATCACCAAGGCGCT-CCAGTATCCCGGCT	3544	QY	1575	SerSerSerLysAlaSerGlnAspArgLysLeuThrSerThrProArgGluIleAlaLys	1594
QY	1218	ProSerAspSerAlaIleThrTyrArgGlySerIleThrHisGlyThrProAlaAspVal	1237	Db	4612	CTATCCAGCAAGCGCTCCAGGACCGGAGTGCATCTACACCCCGGAGATCCCAAG	4671
Db	3545	CGACAGCGGCCCC---AGCTACAGAGGCTCTATCACCCACGC-ACGCCCGCAGACGTC	3597	QY	1595	SerProHisSerThrValProGluHisProHisProIleSerProTyrGluHisLeu	1614
QY	1238	LeuTyrLysGlyThrIleThrArgIleIleGlyGluAspSerProSerArgLeuAspArg	1257	Db	4672	TCCCCACAGACACTGTGCGCGGACCACTCCACCCCATCTCCCGCTATGAGCACTTG	4731
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QY	1258	GlyArgGluAspSerLeuProLysGlyHisValIleTyrGluLysLysGlyHisVal	1277	Db	4732	CTCCGGGCGTCACTGTGTGACCTGTACCGTGTGCATCCCATCCCTGTCCTTTCACCCC	4791
Db	3658	GCACGAGAGGACACCTCGCCCAAGGCGCATCTATATGAGGCAAGAGGCGCACGTC	3717	QY	1635	ThrSerIleProArgGlyIleProLeuAsp---AlaAlaAlaAlaTyrTyrLeuProArg	1653
QY	1278	LeuSerTyrGluGlyGlyMetSerValThrGlnCysSerLysGluAspGlyArgSerSer	1297	Db	4792	ACCTCATACCCCGAGGATCCCTCTGGAAGCAGCAGCGCGCTACTTACCTGCCCGCG	4851
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QY	1298	SerGlyProProHisGluThrAlaAlaProLysArgThrTyrAspMetMetGluLysArg	1317	Db	4852	CACCTTGGCCCCCAGCGCCCACTACCCACACCTGTACCCACCTTACCTCATCCCGCGCTAC	4911
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QY	1338	GluArgHisSerProHisLysLysGlnGlnHisIleArgGlySerIleThrGln	1357	Db	4972	CAGATGACCAACACGCTGCTCCGCCATGGCGCTGCTGACATGCTGAGGGGTCTG	5031
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2492 AlaGlyProHisAlaTrpAspGluGluProLysProLeuLeuCysSerGlnTyrGlu 2511
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US-09-819-104A-4
; Sequence 4, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8544
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)..(7545)
US-09-819-104A-4
Alignment Scores:
Pred. No.: 0 Length: 8544
Score: 10832.50 Matches: 2149
Percent Similarity: 87.94% Conservative: 90
Best Local Similarity: 84.41% Mismatches: 197
Query Match: 81.97% Indels: 117
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QY 21 ProHisSerLeuSerTyrProValGlnLeuAlaArgThrHisThrAspValGlyLeuLeu 40
Db 220 CCCCATGGCATCTCTACCTCCGTCGAGATAGCCGCTCCACACGAGCTGGGGTGTGTT 279
QY 41 GluTyrGlnHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleGln 60
Db 280 GAGTACCAACACACCCCGTGTACTACCTCACACCTGTCTACCCCGTTCATCTCATCAG 339
QY 61 ProGlnArgArgProSerLeuLeuSerGluPheGlnProGlyAsnGluArgSerGln 80
Db 340 CCACAGAGAGGGCGGCTCTACTGTCTCAGAGTTCCAGCTGGGAGTGAACCGGTCTCAG 399
QY 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlySerGluMet 100
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QY 101 GluPheIleGlnSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
Db 460 GAATTCCAGAGGAGCGGCCCGCTGGAGCTACTTACCGATACCCCTGTCTGGCCCA 519

QY 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
Db 520 TCACCCCTGTCTGCCACTTGGGACGCCAGTGGGTCTGAGAGCCTTACCAAGACCGTAGC 579
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Db 580 CTGGCAGGCAAGCTGGAGCCTGTGTCACTCCCGAGTCCCGCCGCGCTACCTGAGCTA 639
QY 161 GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAsn---MetAspArgVal 179
Db 640 GAGCTGGCGCCATCTCGACTGTCCAAGGAGAGCTGATCCAGAACAGATTTGGACCGCGTG 699
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RESULT 9
US-10-087-192-650
; Sequence 650, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2001-03-02
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 650
; LENGTH: 7534
; TYPE: DNA
; ORGANISM: Mus musculus

US-10-087-192-650

Alignment Scores:

Pred. No.: 0 Length: 7534
 Score: 9691.50 Matches: 1893
 Percent Similarity: 87.70% Conservative: 82
 Best Local Similarity: 84.06% Mismatches: 171
 Query Match: 73.34% Indels: 106
 DB: 12 Gaps: 28

US-09-522-753-5 (1-2517) x US-10-087-192-650 (1-7534)

QY 295 LysGlnLysPheCysGlnArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGlu 314
 DB 2 GAACAGCGCTTCTGCGAGCGCTATGACAGCTCATGGAGCGCTGGAGAGAGAGTAGAG 61
 QY 315 ArgIleGluAsnAsnProArgArgAlaLysGluSerLysValArgGluTyrTyrGlu 334
 DB 62 CGCATAGAGAACAAATCCGGAAGGAGGCGCAAGGAGCAGAGTGGAGGACTACGAG 121
 QY 335 LysGlnPheProGluIleArgLysGlnArgGluLeuGlnGluArgMetGlnSerArgVal 354
 DB 122 AAACAGTTCCTCGAGATCCGCAAGCAGCGGAGCTGCAGAGCGCATGCAGAGCGAGGTG 181
 QY 355 GlyGlnArgGlySerGlyLeuSerMetSerAlaAlaArgSerGluHisGluValSerGlu 374
 DB 182 GGCAGCGCTGGAGTGGCTCTCCATGTGGCTGCGCGCAGTGGAGTGGAGTGGAGTGGAG 241
 QY 375 IleLeuAspGlyLeuSerGluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaVal 394
 DB 242 ATCATGATGGCTGTCTGAGCAGGAGAACCTGAGAGCAGATGCGCGAGTGGCGGTG 301
 QY 395 IleProProMetLeuTyrAspAlaAspGlnGlnArgIleLysPheIleAsnMetAsnGlu 414
 DB 302 ATCCCGCCCATGTTGTACGACGCGGACAGCAGAGGATCAAGTTCAATCAATGATGGA 361
 QY 415 LeuMetAlaAspProMetLysValTyrLysAspArgGlnValMetAsnMetTyrSerGlu 434
 DB 362 CTCATGATGATACCCATGAGGCTCTACAGACCGTCAGGTTACCAACATGTGAGCGGAG 421
 QY 435 GlnGluLysGluThrPheArgGluLysPheMetGlnHisProLysAsnPheGlyLeuIle 454
 DB 422 CAGGAGGGACACCTTCCGTGAGAGTATATGAGCAGCACCCTTAAGAACTTTGGCCTGAT 481
 QY 455 AlaSerPheLeuGluArgLysThrValAlaGluCysValLeuTyrTyrTyrLeuThrLys 474
 DB 482 GCCTCATCTCTGGAGAGAAAGCGTCTGAGTGTCTCTCTATTAATCTACCTGACCAAG 541
 QY 475 LysAsnGluAsnTyrLysSerLeuValArgArgSerTyrArgArgArgGlyLysSerGln 494
 DB 542 AAGATGAAATATACAGAGCTTGTGAGCGGAGCTATCGGCGCGCTGGCAAGAGCCAG 601
 QY 495 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 514
 DB 602 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 649
 QY 515 SerSerGlnGluGluLysAspGlyLysGluLysGluLysGluLysGluLysGluLysGlu 534
 DB 650 AGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 709
 QY 535 LysProGluValGluAsnAspLysGluAspLeuLeuLysGluLysThrAspAspThrSer 554
 DB 710 AAGCAGGATGCGAGAACAGAGAGAGAACTCAGCAAGGAGAGAGAGAGAGAGAGAG 769
 QY 555 GlyGluAspAsnAspGluLysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSer 574
 DB 770 GCGCAGGACACGATGAGAGAGAGCGCTGGCTCCAAAGCGCGCAAACTGCCAACAGC 829
 QY 575 GlnGlyArgArgLysGlyArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluGlu 594
 DB 830 CAAGCGCCCGCAAGAGCGTATACGCGCTCCATGGCCCAACGAGGCGCAACCATGAGGAG 889
 QY 595 AlaIleThrProGlnGlnSerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArg 614

DB 890 ACAGCCACCCACAGCAAGTTCCAGAGCTGGCTTCCATGAGATGAACGAGAGTTCTCGC 949
 QY 615 TrpThrGluGluGluMetGluThrAlaLysLysLysGlyLeuLeuGluHisGlyArgAsnTyr 634
 DB 950 TGGACTGAGGAAGAGATGGAGCAGCAAGAAAGGCGCTCTCGAAACATGGAGGAACTGG 1009
 QY 635 SerAlaIleAlaArgMetValGlySerLysThrValSerGlnCysLysAsnPheTyrPhe 654
 DB 1010 TCAGCCATTGCCCGCATGTGGCTCCAGACCGTGTCCAGTGAAGAACTTCTACTTC 1069
 QY 655 AsnTyrLysLysArgGlnAsnLeuAspGluIleLeuGlnGlnHisLysLysLeuLysMetGlu 674
 DB 1070 AACTACAAAGAGAGCGCAACCTGGACGAATCTTCAGCAGCAACAAGCTAAAGATGGAG 1129
 QY 675 LysGluArgAsnAlaArgArgLysLysLysLysAlaProAlaAlaSerGluGluAla 694
 DB 1130 AAGAGAGGAAACGCTCGGAGGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1189
 QY 695 AlaPheProValValGluAspGluGluMetGluAlaSerGlyValSerGlyAsnGlu 714
 DB 1190 GCCTTCCACCTGCGCTGAG 1249
 QY 715 GluGluMetValGluGluAlaGluAlaLeuHisAlaSerGlyAsnGluValProArg 733
 DB 1250 GAAGAGCTGGCGGAGGAG 1309
 QY 734 GlyGluCysSerGlyProAlaThrValAsnAsnSerSerAspThrGluSerIleProSer 753
 DB 1310 GGGAGTGCAGTGGCGGAG 1369
 QY 754 ProHisThrGluAlaAlaLysAspThrGlyGlnAsnGlyProLysProProAlaThr 772
 DB 1370 CCGCGTTTCAGAGCGCAGCAG 1420
 QY 773 LeuGlyAlaAspGlyProProGlyProProThrProThrProThrProThrProThr 791
 DB 1421 GCATTCGCGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1474
 QY 792 AlaProIleGluProThrProAlaSerGluAlaThrGlyAlaProThrProProProAla 811
 DB 1475 GCGCTGTGTGAGCGCTCCCGAGTCCCTGATGCGAGTGGCGCCAGCAGCAGCAGCAGCAG 1534
 QY 812 ProProSerProSerAlaProProValProValProLysGluGluLysGluGluGluThr 831
 DB 1535 CCATCATCTCCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1591
 QY 832 AlaAlaAlaProValGluGluGlyGluGluGlnLysProProAlaAlaGluGluLeu 851
 DB 1592 GCTTCAGCTCCCGCAGCAGAGAGATGCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1645
 QY 852 AlaValAspThrGlyLysAlaGluProProProProProProProProProProProPro 862
 DB 1646 ATCATGTGGAG 1702
 QY 863 LysSerGluCysThrGluGluAlaGluGluGlyProAlaLysGlyLysAspAlaGlu 881
 DB 1703 AAGAGTGCACAG 1762
 QY 882 AlaAlaGluAlaThrAlaGluGlyAlaLeuLysAlaGluLysLysGluGlyGlySerGly 901
 DB 1763 GCCATTGAAACTGTGTCTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1816
 QY 902 ArgAlaThrThrAlaLysSerSerGlyAlaProGlnAspSerSerSerAlaThr 920
 DB 1817 GCAGCTGTGACCAAGAGGTTCCAGTCCAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1876
 QY 921 CysSerAlaAspGluValAspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerPro 940
 DB 1877 TGAGTGGCAGTGGTGGAG 1936
 QY 941 ArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSerProGlnLysPro 960

Db	1937	AGGCCCGACCTCTCACC	CCCCCGGCTGGAGATCCC	CGGGCCAGTACTCTCG	CCCCCAGAACGC	G	1999
Qy	961	LeuAspLeuLysGlnLeuLysGlnArgAlaAlaIleProProfileGlnValThrLys				Lys	980
Db	1997	CTGGACCTGAAGCAGCTGAAGCAGGAGCAGCGCCCATCCCCCTATC---	GTCACCAAG	2053			
Qy	981	ValHisGluProProArgGluaspAlaAlaProThrLysProAlaProProAlaProPro	1000				
Db	2054	GTCCATGAGCCCCCGGGAGCACACAGTACCCCCAAAGCCAGTTCCCTTGCTGCC	TCCA	2113			
Qy	1001	ProProGlnAsnLeuGlnProGlnSerAspAlaProGlnGlnProGlnLysSerSerProArg	1020				
Db	2114	CCCCAGCAGACCTTACAGCAGAGGGTGACGTGCTCAGCAGTCGGGAGGAAGTCCACGT	2173				
Qy	1021	GlyLysSerArgSerProAlaProProAlaAspLysGlu-----	1033				
Db	2174	GGCAAGTCCCGACGCCAGTCCTCTCTGCCGAGAAGAGGCAGAGAACCCGCATTC	2233				
Qy	1034	---AlaPheAlaAlaGluAlaGlnLysLeuProGlyAspProProCysTrpThrSerGly	1052				
Db	2234	CCGGCTTCCCAA	CTGAGGGCCCAAAGCTACCGACTGAGCCCCACGCTGTCATCGGCG	2293			
Qy	1053	LeuProPheProValProProArgGluValIleLysAlaSerProHisAlaAlaProAspPro	1072				
Db	2294	CTGCCCTTCCCCATCTCCACGGGAGGTGATCAAGACTTCCCCACA	CGCGCTGACCCC	2353			
Qy	1073	SerAlaPheSerTyAlaProProGlyHisProLeuProLeuGlyLeuHisAspThrAla	1092				
Db	2354	TCTGCTTCTCCTACACACCCCCCGGTACCCCGTGCCTCTGGGCCCTCCAGATAGTGCC	2413				
Qy	1093	ArgProValLeuProArgProProThrIleSerAsnProProProLeuilleSerSerAla	1112				
Db	2414	CGGCCCGTCTCTGCCACGTCCCCCC--ATCTCTAA	CCCCCCCCCATCTCTCTCTGCC	2470			
Qy	1113	LysHisProSerValLeuGluArgGlnIleGlyAlaIleSerGlnGlyMetSerValGln	1132				
Db	2471	AAGCATCCCGCGTACTTGAAGAGCAGCATGGGTGCCATCTCCCAGGGGATGT	CAGTCCAG	2530			
Qy	1133	LeuHisValProTyrSerGluHisAlaLysAlaProValGlyProValThrMetGlyLeu	1152				
Db	2531	CTTCGTGTGCTCTACTCAGACATGCCAAGCCCCCATGGGCCCTCTCACCATGGGGCTG	2590				
Qy	1153	ProLeuProMetAspProLysLysLeuAlaProPheSerGlyValLysGlnGluInLeu	1172				
Db	2591	CCCCCTTGGCGGGACCTTAAGAAGCTG-----	2617				
Qy	1173	SerProArgGlyGlnAlaGlyProProGluSerLeuGlyValProThrAlaGlnGluAla	1192				
Db	2617	-----	2617				
Qy	1193	SerValLeuArgGlyThrAlaLeuGlySerValProGlyGlySerIleThrLysGlyIle	1212				
Db	2618	-----GGGACAGCACTGGGCTCGGCCAC	CAGTAGTGAAGCATCACCAAGGGCCCTC	2665			
Qy	1213	ProSerThrArgValProSerAspSerAlaIleThrTyArgGlySerIleThrHisGly	1232				
Db	2666	CCCACTACCCGGGTGCAGACGGCCCC-----AGCTACAGAGGCTCTATCATCCCCACGGC	2719				
Qy	1233	ThrProAlaAspValLeuTyTyLysGlyThrIleThrArgIleIleGlyGluAspSerPro	1252				
Db	2720	ACGCCCCGAGAGCTCTCTACAAGGGTACCATCAGCAGGATCGTCGGTGGAGGACAGCCCA	2779				
Qy	1253	SerArgLeuAspArgGlyArgGluAspSerLeuProLysGlyHisValIleTyArgGly	1272				
Db	2780	AGTCGCCTTGACCGGGCAGAGAGCACCCCTGCCCCAAGGGCCATGTCATCTATGAGGGC	2839				
Qy	1273	LysLysGlyHisValLeuSerTyTyGluGlyMetSerValThrGlnCysSerLysGlu	1292				
Db	2840	AAGAAAGCCACGTCTCTATCTATGAGGTGTATGTCCGTGTCTACAGTGTCTTAGGAG	2899				
Qy	1293	AspGlyArgSerSerGlyProProHisGluThrAlaAlaProLysArgThrTyAsp	1312				
Db	2900	GATGCAAGGACAGCTCGGGCCACCCCATGAGACTCGCGCCCTAAACCAACCATATGAC	2959				

QY	1313	MetMetGluGlyArgValGlyArgAlaIleSerSerIleGluGlyLeuMetGly	1332
DB	2960	ATGATGAGGGCCGTGTAGGCAGACTGTTCACCTCAGCCAGCATAGAGGACTCATGGC	3019
QY	1333	ArgAlaIleProProGluArgHisSerProHisHisLeuLysGluGlnHisIleArg	1352
DB	3020	CGCCCATC---CTGAGACGACAGGCC---CACCTCAAGGAGCAGCATCATCCGA	3073
QY	1353	GlySerIleThrGlnGlnIleProArgSerTyrValGluAlaGlnGluAspTyrLeuArg	1372
DB	3074	GGCTCCATCAGCAAGGCATCCCGAGTCTCTATGTGGAGGCGCAGGAGACTACTTACGG	3133
QY	1373	ArgGluAlaLysLeuLeuLysArgGluGlyThrProProProProProProSerArgAsp	1392
DB	3134	CGGAGGCCAAGCTCTTGAAGCGACAAGGACACACACACCCACACCTCGCGEAC	3193
QY	1393	LeuThrGluAlaTyrLysThrGln-----AlaLeuGlyProLeuLysLeuLysPro	1409
DB	3194	CTGACTGAGACCTTACAAGCCCGCCCTCGAACCTCTGGGTCCCTTGAAGCTGAAGCCG	3253
QY	1410	AlaHisGluGlyLeuValAlaThrValLysGluAlaGlyArgSerIleHisGluIlePro	1429
DB	3254	ACTCACAGGGTGTGTAGCACTGTGAAGAGCGCGCGCTCTATCCATGAGATCCG	3313
QY	1430	ArgGluGluLeuArgHisThrProGluLeuProLeuAlaProArgProLeuLysGluGly	1449
DB	3314	AGAGAGAGCTGCGCCGCACACCTGAGCTACCCCTGGCACACGCGCTCTGAAGAGGGT	3373
QY	1450	SerIleThrGlnGlyThrProLeuLysTyrAspThrGlyAlaSerThrThrGlySerLys	1469
DB	3374	TCCATCACCCAGGCGACCCCACTCAAGTAGCACTCTGGGCGACCTCCACTGGCACCAG	3433
QY	1470	LysHisAspValArgSerLeuIleGlySerProGlyArgThrPheProProValHisPro	1489
DB	3434	AAACACAGCTGCGCTCATCATCGGAGCCCGCGCGCTTTCCTTGCCTGCACCGC	3493
QY	1490	LeuAspValMetAlaAspAlaArgAlaLeuGluArgAlaCysTyrGluGluSerLeuLys	1509
DB	3494	CTGCACATAATGGCTGATGTCGCGGCACCTGGAGCGTCCCTGCTATGAAGAGAGTCTGAAG	3553
QY	1510	SerArgProGlyThrAlaSerSerSerGlyCysSerIleAlaArgGlyAlaProValIle	1529
DB	3554	AGCCGGTCAGGGACCGACAGTGTGTGAGGGGGCTCCATCACACGTGGGGGTCCAGTCGTC	3613
QY	1530	ValProGluLeuGlyLysProArgGlnSerProLeuThrTyrGluAspHisGlyAlaPro	1549
DB	3614	GTGGCTGAACCTGGGCAAGCACCGCAAGGCCACTGTACTTACGAAGACCAACGCGGACCC	3673
QY	1550	PheAlaGlyHisLeuProArgGlySerProValThrMetArgGluProThrProArgLeu	1569
DB	3674	TTACACAGTCACTGCCACGTGGCTCCCTGTGACCAAGGGGAGCCACGCGCAGCGCTT	3733
QY	1570	GlnGluGlySerLeuSerSerSerLysAlaSerGlnAspArgLysLeuThrSerThrPro	1599
DB	3734	CAGGAAGGCGAGCTCTTATCCAGCAAGCGCTCCCGAGCACCGAAGCTGACATCTACACCC	3793
QY	1590	ArgGluIleAlaLysSerProHisSerThrValProGluHisHisProHisProIleSer	1609
DB	3794	CGGAGATCGCCAACTGCCACACAGACACTGTGCCCGGAGCACCAACCTCAACCCATCTCC	3853
QY	1610	ProTyrGluHisLeuLeuArgGlyValSerGlyValAspLeuTyrArgSerHisIlePro	1629
DB	3854	CCCTATGAGCACTTGCTCCGGGGCGTGACTGGGTGTGACCTGTATACCTGGTGCATATCCA	3913
QY	1630	LeuAlaPheAspProThrSerIleProArgGlyIleProLeuAsp---AlaAlaAlaAla	1648
DB	3914	TTGGCTTTTGACCCCACTCATACCCCGAGGATCTCTTGGGAAGCAGCAGCGCGCAGCC	3973
QY	1649	TyrTyrLeuProProArgHisLeuAlaProAsnProThrTyrProHisLeuTyrProProTyr	1668
DB	3974	TACTACTCTGCCCGGCACTTGGCCCGACCGCCCACTTACCACACCTGTATCCCACTTAC	4033

QY	1669	LeuIleArgGlyTyrProAspThrAlaAlaLeuGluAenArgGlnThrIleIleAsnAsp	1688	Db	5054	TAAACCCCTTTTCCATCCAGGAATTTGGAATCGGTTCTCTGGGTACACAGTGGAGCTGG	5113
Db	4034	CTCATCCGCGGTACCTGACACGGCGGCTTGGAGAACCGCAGACCATCATCAATGAC	4093	QY	2047	rTyrSerProGluGlyValGluProValSerProValSerSerProSerLeuThrHisAs	2067
QY	1689	TyrIleThrSerGlnGlnMetHisHisAsnThrAlaThrAlaMetAlaGlnArgAlaAsp	1708	Db	5114	CTACAGCCCGATGGGTGGAGCCCATCAGCCGGTGGAGCTCCCGCCAGCTGACCCACGA	5173
Db	4094	TACATCACCTCGCAGCAGATGACCAACACGCTCGCCTCGCCATGCGCCAGCGTCTGAC	4153	QY	2067	plyGlyLeuProlyshisLeuGluLeuAspLysSerHisLeuGluGlyGluLeuAr	2087
QY	1709	MetLeuArgGlyLeuSerProArgGluSerSerLeuAlaLeuAsnTyrAlaAlaGlyPro	1728	Db	5174	CAAGGGGCTCTCCAAACCTCTGGAAGAGCTAGAGAGAGCCACTTGGAGGGGAGCTGCG	5233
Db	4154	ATGCTGAGGGGTCTGTCACCGGAGAGTCTCGCTGGCCCTCAATTAATGCGCTGGCCCA	4213	QY	2087	gProLysGlnProGlyProValLysLeuGlyGlyAlaAlaHisLeuProHisLeuAr	2107
QY	1729	ArgGlyIleIleAspLeuSerGlnValProHisLeuProValLeuValProProThrPro	1748	Db	5234	GCACAGCAGCAGCCGCCCATGAAGCTCAGCGCGAGGCTGCCCATCTCCACATCTGCG	5293
Db	4214	AGAGGCATTATCGACCTGCCACCGCATCGACACCTGCGCGTGTGTGTGCACCAACGCA	4273	QY	2107	gProLeuProGluSerGlnProSerSerProLeuLeuGlnThrAlaProGlyValLys	2127
QY	1749	GlyThrProAlaThrAlaMetAspArgLeuAlaTyrLeuProThrAlaProGlnProPhe	1768	Db	5294	GCCACTGCGCAGAGCCAGCCCTCATCCAGCCCACTCTCTCAGACTGCCCCAGGCATCA	5353
Db	4274	GGCACCCCTGCCACCGCATCGACCGCTTGCTACTCTCCCACTGGCGCCCACTCTC	4333	QY	2127	sglyHisGlnArgValValThrLeuAlaGlnHisIleSerGluValIleThrGlnAspTy	2147
QY	1769	SerSerArgHisSerSerProLeuSerProGlyGlyProThrHisLeuThrLysPro	1788	Db	5354	AGGTACACAGAGGTGTGTACCCCTGGCTCAGCACATCAGCGAGTCTATTACCGAGGACT	5413
Db	4334	AGCAGCGCCACAGTAGTACCTCACCGTGTCCAGAGAGGCCCACTCACCTAGCTAAACCA	4393	QY	2147	rThrArgHisHisProGlnGlnLeuSerAlaProLeuProAlaProLeuTyrSerPhePr	2167
QY	1789	ThrThrThrSerSerGluArgGluArgAspArgAspArgGluArgAspArgAspArg	1808	Db	5414	CACGCGCCACCAACCGCAGCAGCTCAGTGGCCCTTCCCGCCCTCTCTACTCTCTTTC	5473
Db	4394	ACTGCCACATCTTTCATCGGAGCGGGAACGGGAACGTGAGCGGGAACGAGAC	4444	QY	2167	oGlyAlaSerCysProValLeuAspLeuArgProProSerAspLeuTyrLeuProPr	2187
QY	1809	GluArgGluLysSerIleLeuThrSerThrThrValGluHisAlaProIleThrArg	1828	Db	5474	CGAGGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5533
Db	4445	-----AAGTCCATCTCAGTCTACCACTACAGTGAGCATGCCATCTGGAGA	4495	QY	2187	oProAspHisGlyAlaProAlaArgGlySerProHisSerGluGlyGlyLysArgSerPr	2207
QY	1829	ProGlyThrGluGlnSerSerGlySerSerGlySerSerGlyGlyGlyGlySerSer	1848	Db	5534	CCCCCACCATGCGACCCCGGGGATCCCCCAGAGTGAAGGGGCAAAAGTCCCC	5593
Db	4496	CCTGGTACGAGCAGACGAGCGGGCT-----GGGGGCGAG	4531	QY	2207	oGluProAsnLysThrSerValLeuGlyGlyGlyGluAspGlyIleGluProValSerPr	2227
QY	1849	SerArgProAlaSerHisSerHisAlaHisGlnHisSerProIleSerProArgThrGln	1868	Db	5594	AGAACCACCAAAACATCGTCTCGGAGCAGCATGCTCGGAGCGCTGTGTACCCACTGCTGTATCG	5713
Db	4532	AGCGCGCGCGCTCCACACC-----CACAGCACTCGGCCCATCTCCCCCGGACCCAG	4585	QY	2247	gAspGlyGluGlnThrGluProSerArgMetGlySerLysSerProGlyAsnThrSerGl	2267
QY	1869	AspAlaLeuGlnGlnArgProSerValLeuHisAsnThrGlyMetLysGlyIleIleThr	1888	Db	5714	AGACGGGGAACAGGGCGAGCCCC---AGGATGGGCTCTAAGTCTCCAGGCAACACCCAGCCA	5770
Db	4586	GACCGCTTGACAGAGAGGCCAGTGTCTGCACAAACAGCAGCATGAAGGGCGTGGTCACC	4645	QY	2267	nProProAlaPhePheSerLysLeuThrGluSerAsnSerAlaMetValLysSerLysly	2287
QY	1889	Ala-ValGluProSerLysProThrValLeuArgSerThrSerThrSerSerProValAr	1908	Db	5831	GCAGGAGATCAACAGAAACTCAACACCACCAACCGGAACAGCAGCAGATACATAATTGG	5890
Db	4646	TCCCGTGGAAACCCGGCAGCGCCAGTGTCTGCACAAACAGCAGCATGAAGGGCGTGGTCCG	4705	QY	2307	rGlnProGlyThrGluIlePheAsnMetProAlaIleThrGlyThrGlyLeuMetThrTy	2327
QY	1908	gProAlaAlaThrPheProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyWa	1928	Db	5891	CCAGCCTCGGAGCGAAATCTTCAACATGCCCGCCATCTCTGAGCAGCGGCTTATGACCTG	5950
Db	4706	CCGAGCTGCCACATTCACCTGCGCCACCCACTGCGCCACTTGGTGGCACCTTGAAGGGGT	4765	QY	2327	rArgSerGlnAlaValGlnGluHisAlaSerThrAsnMetGlyLeuGluAlaIleIleAr	2347
QY	1928	lTyrProThrLeuMetGluProValLeuLeuProLysGluAlaProArgValAlaArgPr	1948	Db	5951	TAGAGCCAGGCGGTGCAAGNACACCCAGCACCACATACATGGGCTAGAGGCCATTATTAG	6010
Db	4766	CTACCTACCTCATCGAGCGCGTCTGTATACCAAGAGACCTCTCGGGTCGCGCCGCCC	4825	QY	2347	glyAlaLeuMetGlyLysTyrAspGlnTrpGluGluSerProProLeuSerAlaAsnAl	2367
QY	1948	oGluArgProAlaAspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGl	1968	Db	6011	AAAGGCACCTCATGGTAAATATGATCAGTGGGAAGAGCCCGCCCTCGGCGCCAATGC	6070
Db	4826	CGAGCGGCGCGGTGGAGCGCTGGCCATGCTTCTTACCAAAACCCCGGCGCCG	4880	QY	2367	aPheAsnProLeuAsnAlaSerAlaSerLeuPro---AlaAlaMetProIleThrAlaAl	2386
QY	1968	yLeuGluProAlaSerProSerLysGlySerGluProArgProLeuValProProVa	1988	Db	6130	TTTTAACCTCTGAAATGCCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6130
Db	4881	---GAGCGCGCTCTCACCAGCAGAGCTCCGAGCCCGCATCCCTTAGCACCCCCCGAG	4936	QY	2386	aAspGlyArgSerAspHisThrLeuThrSerProGlyGlyGlyLysAlaLysValSe	2406
QY	1988	lSerGlyHisAlaThrIleAlaArgThrProAlaLysAsnLeuAlaProHisHisAlaSe	2008	Db			
Db	4937	CTCCAGCCACACAGCCATCGCGCGCACCCAGCAAGAGCGCTTGACCCCAACCATGCCAG	4996	QY			
QY	2008	rProAspProAlaProProAlaSerAlaSerAspProHisArgGluLysThrGlnSe	2028	Db			
Db	4997	TCCGAGACCGCGCGG---CCACCTCGCGCTCAGATCTGCACCCAGAGAAAGACTCAAAG	5053	QY			
QY	2028	rLysProPheSerIleGlnGluLeuGluLeuArgSerLeuGlyTyrHis---GlySerSe	2047				

Db 243 TTGACCCCACTCCATACCCCGCGCATCCCTCTGGACGAGCGCTGCTACTACTG 302
Qy ProArgHisLeuAlaProAsnProThrTyrProHisLeuTyrProTyrLeuIleArg 1671
Db 303 CCCGACACTCTGGCCCCCAACCCCACTACCGGACCTGTACCCACCTACTCTCCG 362
Qy GlyTyrProAspThrAlaAlaLeuGluAsnArgGlnThrIleLeuAsnAspTyrIleThr 1691
Db 363 GGCTACCCCGACACCGCGCGCTGGAGAACCGGACAGACCATCATCAATGACTACAC 422
Qy SerGlnMetHisHisAsnThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArg 1711
Db 423 TCGCAGCAGATGACACCAACGCGGCCACCGCCATGCGCCAGAGCTGATATGCTGAG 482
Qy GlyLeuSerProArgGluSerSerLeuAlaLeuAsnTyrAlaAlaGlyProArgGlyIle 1731
Db 483 GGCCTCTCGCCCCGAGTCTCTCGCTGGCACTCACTACGCTGGGGTCCCGAGGCATC 542
Qy IleAspLeuSerGlnValProHisLeuProValLeuValProProThrProGlyThrPro 1751
Db 543 ATCGACCTGTCCCAAGTGCCACACCTGCTGTGCTCGTCCGCCACACAGGACCCCA 602
Qy AlaThrAlaMetAspArgLeuAlaTyrLeuProThrAlaProGlnProPheSerSerArg 1771
Db 603 GCCACCCCAATGGACCGCTTGCTTACCTCCCAACCGCGCCCGCCCTTCAGACGCG 662
Qy HisSerSerProLeuSerProGlyGlyProThrHisLeuThrLysProThrThrThr 1791
Db 663 CACAGAGCTTCCCACTCTCCCAAGAGGTCCAAACACACTTGACAAACACACACAG 722
Qy SerSerSerGluArgGluArgAspArgAspArgGluArgAspArgGluArgGlu 1811
Db 723 TCCTCGTCCGAGCGGAGCGAGACCGGGATCGAGACGGGATCGGGAGCGGAA 782
Qy LysSerIleLeuThrSerThrThrThrValGluHisAlaProIleThrArgProGlyThr 1831
Db 783 AAGTCCATCTCAGCTCCACACAGCGTGAGACACGCCCATCTCGAGACCTGGTACA 842
Qy GluGlnSerSerGlySerSerGlySerGlyGlyGlyGlyGlySerSerSerArgPro 1851
Db 843 GAGCAGACGCGGACGAGCGGCGAGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGG 902
Qy AlaSerHisSerHisAlaHisGlnHisSerProHisSerProArgThrGlnAspAlaLeu 1871
Db 903 GCCTCCCACTCCCACTCCCAACGACACTCGGCCATCTCCCTCGGACCCAGAGTGCCTC 962
Qy GlnGlnArgProSerValLeuHisAsnThrGlyMetLysGlyIleIleThrAlaValGlu 1891
Db 963 CAGCAGACGCCAGTGTGCTTCAACACAGGCAATGAAGGGTATCATCACCGCTGTGGAG 1022
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Db 1023 CCAGACGCGCCAGCTCTGAGGTCCACCTCCACCTCTCTCACCCGTTCCGCCAGCTGCC 1082
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Db 1083 ACATTCCACCTGCCACCCCACTGCCCCACTGGCGGCACCTCGATGGGTCTACCTACC 1142
Qy LeuMetGluProValLeuLeuProLysGluAlaProArgValAlaAlaArgProGluArgPro 1951
Db 1143 CTCATGAGCGCGCTTGTGCTGCCAAGGAGCGCCCCCGGGTCCGCCAGAGCGGCC 1202
Qy ArgAlaAspThrGlyHisAlaPheLeuAlaLysProAlaArgSerGlyLeuGluPro 1971
Db 1203 CGAGCAGACACCGGCCATGCTTCTCTGCCAAGCCCCCGAGCCGCTCCGGGCTGGAGCCC 1262
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Db 1263 GCCTCTCTCCCGACAGGCGCTGGAGCCCCCGGCCCTTAGTGCTCTCTCTCTGGCCAC 1322
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Qy ProValLeuAspLeuArgArgProProSerAspLeuTyrLeuProProProAspHisGly 2191
Db 1863 CCGTCTCTGAGCTTCCGCGCCCGCCACCCAGTGACCTCTACTCTCTCTCTCTCTCTCT 1922
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Db 2402 ----- 2402

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1468	GCAGAACAAAGACGAGTCAAGTTCATTAACATGATGGCTTATGGAGGACCTATGAA	1527
422	ValTyrLysAspArgGlnValMetAsnMetTrpSerGluGlnGluLysGluThrPheArg	441
1528	GTGTATTAAGATAGCCAGTTTATCAATGTTTGGACTGACCATGAAAGAGAGATCTTTAAG	1587
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1588	GACAAGTTTATCCAGCATCAAAAACCTTTGGACTAATTCATCATCATCTTGGAGAGGAAG	1647
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1768	CAAGAGAAAAGTAGAGAAAAAAGAGG-----GATAAAGCAGAAAAAAGACAAAAA	1821
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1822	AAAGAGAGAAAGAAAGATGAGAGGAAAGATGAAAGAGAAAGAGACTCCAAGAAAT	1881
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Qy	2421	LeuAlaSerGlyAspArgProProSerValSerSerValHisSerGluGlyAspCysAsn	2440
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Qy	2441	AtcArgThrProLeuThrAsnArgValTrrGluAspArgProSerSerAlaGlySerThr	2460
Db	7330	AGGCACAGCGCCA-----GGTGGCGCTGGGAAGACAGGCCCTCTTCAACAGGCTCAACT	7383
Qy	2461	ProPheProTyrAsnProLeuLeuMetArgLeuGlnAlaGlyValMetAlaSerProPro	2480
Db	7384	CAGTTTCCCTTATAACCTCTGACTATGGGATG-----CTCAGCAGTACTCCACCA	7434
Qy	2481	ProProGlyLeuProHlaGlySerGly--ProLeuAlaGlyProHis-----His	2496
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Qy	2497	AlaTrrAspGluGluProLysProLeuLeuCysSerGlnTrrGluThrLeuSerAspSer	2516
Db	7495	ATCTGGGAGCGAGAGCTGCCCCACTGCTCTCAGCACAGTAGTACGAGACCTGTCCGATAGT	7554
Qy	2517	Glu 2517	
Db	7555	GAT 7557	
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; Sequence 649, Application US/10087192			
; Publication No. US20020182586A1			
; GENERAL INFORMATION:			
; APPLICANT: Morris, David W.			
; APPLICANT: Engelhard, Eric K.			
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR			
; TITLE OF INVENTION: CANCER			
; FILE REFERENCE: 529452000122			
; CURRENT APPLICATION NUMBER: US/10/087,192			
; CURRENT FILING DATE: 2002-03-01			
; PRIOR APPLICATION NUMBER: US 09/747,377			
; PRIOR FILING DATE: 2000-12-22			
; PRIOR APPLICATION NUMBER: US 09/798,596			
; PRIOR FILING DATE: 2001-03-02			
; NUMBER OF SEQ ID NOS: 2059			
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; ORGANISM: Mus musculus			
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; OTHER INFORMATION: n = A,T,C or G			
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Best Local Similarity: 18.73% Mismatches: 234			
Query Match: 27.61% Indels: 5797			
DB: 12 Gaps: 57			
US-09-522-753-5 (1-2517) x US-10-087-192-649 (1-91141)			
Qy	694	AlaAlaPheProValValGluAspGluGluMetGluAlaSerGlyValSerGlyAsn	713
Db	57918	GCTGGGGCTCCAGCTTCTCGAGAGACAGCTTAGACTGTATCGAGGTGATCCGGGAAC	57977
Qy	714	GluGluGluMetValGluGluAlaLeuHisAlaSerGlyAsnGluValProArg	733
Db	57978	CCTTAGCTGTCAGTT-----TCTGTTCCAGG	58004

Qy	734	GlyGluCysSerGlyProAlaThrValAsnAsnSerSerAspThrGluSerIleProSer	753
Db	58005	 TCAGGCGCAGTA	58040
Qy	754	ProHisThrGluAlaAlaLysAspThrGlyGlnAsnGlyProLysProProAlaThrLeu	773
Db	58041	 CCAGGCGTT--GCAGCTCAGAACAGATGGCAGCTAAAGCCAGAGCTTGTA--AGCTC	58095
Qy	774	GlyAlaAspGlyProProGlyProProThrProProProArgThrSerArgAlaPro	793
Db	58096	 AGTGAGTGTGGCGTGTCTCTGGGTGTCAACACCT-----GAAAGTCACAGGGGACCT	58149
Qy	794	IleGluProThrProAlaSerGluAlaThrGlyAlaProThrProProAla-----	811
Db	58150	 GAGCCTGTGGCACACGCCATGGGCACAGGCCATGGCTGGAGCCAGCTGCTCGGTT	58206
Qy	812	ProProSerProSerAlaProProProValValProLysGluGluLysGlu	828
Db	58207	 CTCAGGTCTCCCTGCAGCTCAGCAGCTGGGGCTCAGTCTTCCCATCTGG--AGGCTGAAG	58265
Qy	829	GluLThrAlaAlaAla-----	836
Db	58266	 GAACAGACTGGCTGCATCCGAAACAGTGTACTTTTGTGTTTGTGGCCA--	58322
Qy	837	ValGluGluGluGluGlnLysProProAlaAlaGluGluLeuAlaValAspThr---	855
Db	58323	 -----CATGGGTCCAATCAGACATGGCCATATTGGCAGGTGACCGAAGAGACCTGA	58376
Qy	856	GlyLysAlaGluGluProValLysSerGluCysThrGluGluAlaGluGluGly	873
Db	58377	 TCAATGGGTGGTCACTGCTCT-----CAGTGTACCTTACAGCTCATCAAGGC	58427
Qy	874	ProAlaLysGlyLysAspAlaGluAlaAlaGluAlaThrAlaGluGlyAlaLeuLysAla	893
Db	58428	 CCGGCT-----GGAGCTCAGCTAGT	58448
Qy	894	GluLysLysGluGlyGlySerGlyArgAlaThrThrAlaLysSerSerGlyAlaProGln	913
Db	58449	 GACCAG-----TATAGTAGATG--GTAGGCGCACAGACTGCCTCTCCCATGC	58495
Qy	914	AspSerAspSerAla-----ThrCysSerAlaAspGluVal	926
Db	58496	 TCATCTAGATGACTGCTATTAAGCACCATCATTTGGCAGAACCTGGCAGC-----	58543
Qy	927	AspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerProArgProSerLeuThr	946
Db	58544	 -----CAGGAGGGCGAGCAA-----GCCTGACCCAGCACTCTTGT	58579
Qy	947	ProThrGlyAspProArgAlaAsnAlaSerProGlnLysProLeuAspLysGlnLeu	966
Db	58580	 CCT-----ATACATCCAGCTGGTGGCAATCTCGCGGGAAACCGTG	58618
Qy	967	LysGlnArgAlaAlaAlaAlaProProIleGlnValThrLysValHisGluProProArg	986
Db	58619	 AAGCAAGATCAGCCCTC-----	58636
Qy	987	GluAspAlaAlaProThrLysProAlaProProAlaProProProGlnAsnLeuGln	1006
Db	58637	 TGACACATGGCCCTGTGTGTGCTCTCCCTGTGTGTCTGGCCATGAGCCAGCTCATACCA	58696
Qy	1006	nProGluSer-----AspAlaProGlnGlnProGly--	1016
Db	58697	 AGCAGGTAGCATGGGAACGTAGCAGCACACTCACTGACTCTGTCCAGCACCCCTCTTG	58755
Qy	1017	-----SerSerPro--	1019
Db	58757	TCAGGTCCTGTGCACAGCTTCCAGTGTGTGTGGAGGTATGGAGATGGCAGAGCCCTCC	5881
Qy	1020	-----ArgGlyLysSerArgSerProAlaProProAlaAspLysGluAlaPheAlaAl	1037
Db	58817	 CTGACTGGCCACCTTAATCTTTTTCAGCAGAAACCCGCACTTTCTTCGCGCTTCCCAAC	58871

Qy	1037	aGluAlaGlnLysLeuProGlyAspProCySerThrSerGlyLeuProPheProVa	1057	Db	59957	C---ATCTCTAAACCCCAACCCCTCATCTCTGCAAGCATCCCGCGTACTTGAGAG	60013
Db	58877	TGAGGGCCCAAGACTAGCACTAGAGCCCAACGCTGTGTATCGGGCCCTGCCCTTCCCAT	58936	Qy	1120	gGlnIleGlyAlaIleSer	1126
Qy	1057	lProProArgGluValIleLysAlaSerProHisAlaProAspProSerAlaPheSerTy	1077	Db	60014	GCAGCTGGGTGCCATCTCCACAGGTAGTACTCTCGGGGCTGGGTCTCCCATCACAGGGA	60073
Db	58937	CCCTCCACGGAGGTGATCAAGACTTCCCAACAGCCGCTGACCCCTCTGCCCTTCTCTTA	58996	Qy	1126	-----	1126
Qy	1077	rAlaProPro	1080	Db	60074	GCCTTTTGTAGCCATGGGTGTTTCCAGGATGCTACTGGTGGGAGCCGCTGGGCTCA	60133
Db	58997	CACACCCCGGTGAGTGGACAGCGCACCTTAGTCTGTGCAGTGGTGGGAGCCAA	59056	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60134	TCCCTGCGAGTTGGGCAGCCTACGGGCTACGTGGATCTCAGGCTGTGATTTCCGCTGC	60193
Db	59057	CTCTTTTCAGTGTGCGAGGCTGCATGTGTGCGATCGGATGAGACCTTGGCTGAAGGTGTG	59116	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60194	CTCAGGAGGTGACTCAACGCTCTGGAGGCTCAGTTTCATCTCTGTTTCAGTGAGAGGTG	60253
Db	59117	ACCTGCTCACTCTGTGAAGCTGGGCACCTTCTGAGACTCGGGAAGCTTCGCGACTACC	59176	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60254	GGGAGCTGCAGCTGTACAGGCTATCGAGTGTACAGTCTATAAGCCCTTGGTCACTCTGC	60313
Db	59177	TGCACGGCCATAGCAGCCTTGGAGGAACTTGAGCTGGAAAGGGAGGCCAGCGTGGGA	59236	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60314	ATCCTACTCCCTCAGCACACGGGATCGAGTGTACACTGTGTCTTTACGTGGGC	60373
Db	59237	GCTATTTTCCACCAGTGACTAAGAGGTGTCTATTAGAGGAGCAGTGGGCGTCTTGAT	59296	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60374	ACTGGCCTGGGCGAGTTGTGGCTGTCTCCCATCTCCAGCTGAGTGGGCGGACAGCCC	60433
Db	59297	TGACAGATAGTGTAGAGACTGTTTGGGGGGAAGCCACTAGGTTTCTATTCTTGATGG	59356	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60434	CATCTCTGACCTGCATATCCTTAAGTCCAGAGTGGGCTCTCCCTGTGTCTGAATCTGGT	60493
Db	59357	TCCTTACCACCACTAAAGTAATCCAGCCAGGGGCCAGTGATTAACAGCATCAGCAGTGG	59416	Qy	1127	-----GlnGlyMetSerValGlnLeuHisValProTyrSerG	1139
Qy	1080	-----	1080	Db	60494	TGTGATCTGTTTCTTACCCTTAGCAGGGGATGTCACTCCAGCTTCGTGTGCTCACTCAG	60553
Db	59417	CTGGCCAGGTAGAGCTGACCCATGGCAAGTGTACTGAGGGAGCTTGGAGAACAGGGA	59476	Qy	1139	luHisAlaLysAlaProValGlyProValThrMetGlyLeuProLeuProMetAspProL	1159
Qy	1080	-----	1080	Db	60554	AGATGCCAAGGGCCCCATGGGCCCTCTCACTACATGGGGCTGGCCCTTGGCGTGGACCTTA	60613
Db	59477	AAGGCATGCCAGGAGGAAGAACAGCATAGCATGTGCAAGGGCCAGAACACTCTCGAG	59536	Qy	1159	YsLysLeu	1161
Qy	1080	-----	1080	Db	60614	AGAAGCT-GGGTGAGTTCCCAACACCTTGTGTTCTTACAACCTTGGCTAAGGGTGGGC	60672
Db	59537	TCGGGACACTTGAGGCACCGAGCATCTGTACAGCATTAACATTTCCACCAGCAAGCC	59596	Qy	1162	-----Alap	1163
Qy	1080	-----	1080	Db	60673	AGTCCCTGGTGGGAGGCGCAGCTTGAGACCTCTGTGTATCTCTCACCCCTCCCTAGCCC	60732
Db	59597	CAGGGATCCCAGTCACTGTCACTGGAAATCCAGGCGGAGGTGACTCTCTCTGAAGGCAT	59656	Qy	1163	roPheSerGlyValLysGlnGlnLeuSerProArgGlyGlnAlaGlyProProGluS	1183
Qy	1080	-----	1080	Db	60733	CCCTTCTAGTGAGTGAAGCAGAGAACAGTTGTCCCTCGGGGTGAGGCTGGGCGACCTGAAA	60792
Db	59657	AGGGGGGGATAGCGTCTGACTCTGGGAAAGTCCCTTTGGCCCTGTGAGGAGAACAG	59716	Qy	1183	erLeuGlyValProThrAlaGlnGluAlaSerValLeuArg	1196
Qy	1080	-----	1080	Db	60793	GTCTGGAGTGCCCACTGTCTCAGAGACCTCTGTGTGTGAG-AGGTAAGGCTGGCACAGTC	60851
Db	59717	GATCTAGGGAGGAGTGGAAATCGGGGTGTGGCTTAGAGGCTTGGGTGTGGATCGGGGG	59776	Qy	1196	-----	1196
Qy	1080	-----	1080	Db	60852	ACCTTCACTCTAGAGAGCCTGAAAGCCCACTTTCAGAGCTGTTTCTCATCTCTTGAGAC	60911
Db	59777	TGGGGTGGTGACGGTGCAGCTTCAGAGAAATCCAGGACTGTGGGTTTCCCGTGGAGTGCT	59836	Qy	1196	-----	1196
Qy	1080	-----	1080	Db	60912	ACCAAGAAGACAGTGGTGGCTTTCAGACATGGGGTCTTACAGAGCTGGGTCTTTTGTGTC	60971
Db	59837	CAAGCCACTGAAGCAGACATGTGGAGAGCCCTCAAGAGACACTTCTTATTTCTTGC	59896	Qy	1197	-----GlyThrAlaLeuGlySerValProGlyGlySerIleThrLysGlyIleProSerT	1215
Qy	1081	-GlyHisProLeuProLeuGlyLeuHisAspThrAlaArgProValProArgProPr	1100	Db	60972	TTCTAGGACAGCACTGGGCTCCGCCACAGTGGAGATCAACAGGGGCTCCCCAGTA	61031
Db	59897	AGGTACCCCTGCTCTGGGCTTCCACATAGTAGTGGCCCGCTCTGTCAGTCCCCC	59956	Qy	1215	hrArgValProSerAspSerAlaIleThrTyrArgGlySerIleThrHis	1231
Qy	1100	oThrIleSerAsnProProProLeuIleSerSerAlaLysHisProSerValLeuGluAr	1120				

Db	61032	CCGGGCTGCAGACGCCCC-----AGCTACAGAGGCTCTATCATCCACGCTAGTGCTG	61085
Qy	1231	-----	1231
Db	61086	GGGGCAGGGTGTACGGGCAGACATCCCAAGTGGCTTGGATGGGATGAGAGCACTCCT	61145
Qy	1231	-----	1231
Db	61146	GGGAGACTAGAGACAATGGCTGAATGGTTGATCACTGTCCGTGTGGGTCAAGCCTAGG	61205
Qy	1231	-----	1231
Db	61206	GTGATAAGAGAACAAACGTCCTGTGTCTCTGGCAGTTAGGTGTGGCAGACCAACAC	61265
Qy	1231	-----	1231
Db	61266	AGATAGGNTAGCCAGCTCATACCAAGGCTGTCAAGAGCCACAGGCGATAGAGTGTCTG	61325
Qy	1231	-----	1231
Db	61326	GACTGAGAAAGTTACCTGGGCGCAGGAAGAGAAAGTGTGACATGTTATTATGGCCGGAAG	61385
Qy	1231	-----	1231
Db	61386	AAATAGAGGAGCAGGGGTGGCAGCTGGCTTGACATATCACCAGTCAGGTAGGCATAAGC	61445
Qy	1231	-----	1231
Db	61446	CAGTGTGCGTGCAGACTTAGTACCACCGAGCAGGAAGGATGCGAGTTCACAGCGA	61505
Qy	1231	-----	1231
Db	61506	ACCTGAAGTGTAGCTGAGAGACCTTGTTCATATGAACAGTATGTTATTCGATA	61565
Qy	1231	-----	1231
Db	61566	GCACTCTGGGAGTCTCGAGAGGACGGTGTGGCAGCAGCATTTGGCACTCGGAAGCCA	61625
Qy	1231	-----	1231
Db	61626	GGATGAGAGACATTTGACAAATCGGAGGGAGTTACATGTGTGGTGTGCTCTGTG	61685
Qy	1231	-----	1231
Db	61686	CATGCTTGGGGTGGGGAGTGGTGGGTGTGAGAGTCACCCACAGATCCGGGTGC	61745
Qy	1232	-----GlyThrProAlaAspValLeuTyrIysGlyThrIleThrA	1245
Db	1245	rgIleIleGlyGluAspSerProSerArgLeuAspArgGlyArgGluAspSerLeuProL	1265
Db	61806	GGATCGTGGTGAGGACAGCCCAAGTCCCTTGACCGGGCAGAGAGACACCTTGCCCA	61865
Qy	1265	yGlyHisValIleTyrGluGlyIysGlyHisValLeuSerTyrGlu-----	1281
Db	61866	AGGGCATGTCTATCATGAGGCAAGAAAGGCCACGCTCTATCTCTATGAAGGTGAGGACA	61925
Qy	1281	-----	1281
Db	61926	GAGGACAGACAAACAGAGGCTCTGGCAGTTAGTGGGTGGCTATGCTCTCTCCCT	61985
Qy	1281	-----	1281
Db	61986	TTCTTTCCGTTACAGGATGTCTTTTCTCAAGACAGACATAGCAAGGCCACTGAGAGCAA	62045
Qy	1281	-----	1281
Db	62046	CCACCTTGTAGGCTGAGGCTTAGCAAGCAAGCACAATAGCAGATAGTACTTCCCTGCCAG	62105
Qy	1281	-----	1281
Db	62106	CTCGCCCTGCTGGGAGTGTGTGGAAACCCTTTGTATTAGGAGTCATGAAGACCGGA	62165
Qy	1281	-----	1281
Db	62166	CTGCAACACAGGCCCCAGACAGCCGTTGTGGGTGTCTCCACTTTGTCTGAGAGGGCCCC	62225
Qy	1281	-----	1281
Db	62226	TTGGAGTTGGCTGTAGCTTGACAGAGTTGGGTCTGGGCTTAGGTTTCATGCTCAGGG	62285
Qy	1281	-----	1281
Db	62286	TCCTCTATGAGAAATACCTTCCTGGCCCTGTGAGACAAGGCAGCCCTTGTTAGGGCTGT	62345
Qy	1281	-----	1281
Db	62346	AGGCTCTATAGAGTCTCTTTTAGAACCAAGCAGAGAGCTGAAGTGATATCAGGTCAGGCA	62405
Qy	1281	-----	1281
Db	62406	GGGAGTGAAGTCTCTCTCGAGGCATACAAACCATGATGAGGTGGGGCTGGCTTGGCG	62465
Qy	1281	-----	1281
Db	62466	GTTTCCCTTACATAGGCTGGAAAGCTGGGGCAGCCTTGTAGTGCCTGCACAGGGAAGG	62525
Qy	1281	-----	1281
Db	62526	GCTGTGGCAGAGCCATGCCACCTCTTCTCTGGCTAGAAAACGTAGCCAGTGTACCTAA	62585
Qy	1281	-----	1281
Db	62586	AAGTTGAGAAACCCGCCCTCGGAAAGCATCCCCATACCAAGGCACCCCTACAAACACTCG	62645
Qy	1281	-----	1281
Db	62646	CTGCTTCAGGCTGGGACTGCACCTTCCTATTCTTGAGCCCAAGAGCCCTTAATC	62705
Qy	1281	-----	1281
Db	62706	CTTGAGGTAAAGTGAACCCCGTGTGTCCAGGGAACAAGGGACCAAGCTGCCTCAGGTGC	62765
Qy	1281	-----	1281
Db	62766	CAGCTGCATGTCTGTGTACAGCCCCAAAGAGCTAGTAGAGCACTAGTCACAGCTTGGG	62825
Qy	1281	-----	1281
Db	62826	AGCCTCCAGAGTCTTAGATTGTAACTTCCAGCCTGTCTTTGTGGAGATGGGGTGTCTTA	62885
Qy	1281	-----	1281
Db	62886	TGCGTCTTTTCTGGGGCCAGTGGGTCTGAGGCAGTTCCAGAGTGTCAACCCCGTCAGTCC	62945
Qy	1281	-----	1281
Db	62946	CAGCCCCAGCTGCCACCTTTCTTTACATAATTTCTTTGTATTTCTCATATAGCCAGC	63005
Qy	1281	-----	1281
Db	63006	ATGTTCCAAAGTCAACAGTGAACAAGCCACTGTCTCCTCGCAGCAGAGGCACACCT	63065
Qy	1281	-----	1281
Db	63066	GTAACTGGCTCACATGGTCTTGGACTCACACATATCCACTTGTGCAATGCAGAGCT	63125
Qy	1281	-----	1281
Db	63126	GCAGGCGTGTGGAGGCTTCCCTGCCACTCAGACTGTGTGACATCTTTTAGTGTGCAC	63185
Qy	1281	-----	1281
Db	63186	ATACACCTATGGGTACAGAGCATACCCACCACTTTACAAAGCCCGGTGGGCATGCCCT	63245
Qy	1281	-----	1281

Qy	1281	-----	1281		AGCCAAAGCTCTTGAAGCGAGAAAGGACACACACACCCACCCACCCACCTCGGACCTGA	64319	Db
Db	63246	GCTCTTTCTGCCAATTGAGCTGGTTTGAAGGTCCCATCTGTGGATGGCAGGGCTCCTT	63305		hrGluAlaTyrLysThrGln-----AlaLeuGlyProLeuLysLeuLysProAlaH	1411	Qy
Qy	1281	-----	1281		CTGAGACCTACAAGCCCGGCCCTCGGACCTCTGGGTCCCTGAAAGCTGAAGCCGACTC	64438	Db
Db	63306	CCAGCTCTGCTATTGGCGGGCCCTAGCACCGTGCCTGTATGTGCCAGCCCTTGGAGCCGT	63365		isGluGlyLeuValAlaThrValLysGluAlaGlyArgSerIleHisGluIleProArgG	1431	Qy
Qy	1282	-----	1292		ACCAGGGTGTGGTAGCAACTGTGAAGGAGCGGGCGCTCTATCCATGAGATCCGAGAG	64498	Db
Db	63366	CCACATCGTGTCTTCTCGGGCTCCAGGTGGTATGTCGTGTACAGTGTCTTAAGG	63425		luGluLeuArgHisThrProGluLeuProLeuAlaProArgProLeuLysGluGlySerI	1451	Qy
Qy	1292	luAspGlyArgSerSerGlyProHisGluThrAlaAlaProLysArgThrTyrA	1312		AGGAGCTGCGCCGACACCTGAGCTACCCCTGGCACCACGGCTCTGAAGAGGGTTCCA	64558	Db
Db	63426	AGGATGAAGGAGCAGCTCGGGCCACACCCATGAGACTGCGGCCCTTAAACGCACCTATG	63485		leThr-----	1452	Qy
Qy	1312	spMetMetGluGlyArgValGlyArgAlaIleSerSerAlaSerIleGlu-----	1328		TCAC-CCAGGTACGAGAGTCCAGAGGGGGGCATGGGCAAGCTGGGGGGTGCTAATG	64617	Db
Db	63486	ACATGATGGAGGGCGGTGAGGAGGACTGTACCTCAGCCAGCATAGAGGGTAAGTGTG	63545		-----	1452	Qy
Qy	1328	-----	1328		CTGCCCTCGTTGCATTGGGTTATAAAGTGGGCCAGAGACATCAGCAGCTGGCCCTGGT	64677	Db
Db	63546	CCGCTGTAGCCACTTACCAGGACCGAGCGTGGCCAGGAACCTCCAGGCACCCAGGCCA	63605		-----	1452	Qy
Qy	1328	-----	1328		CACTGACAGTATTGTGAAACCAAGTCTTATGTCCCTAACTTGTCTACTTGTCTGCC	64737	Db
Db	63606	GAATGGAAAAGGAGTGGCTCTTGACAAGCTTGGAGGGATCCAGTTAGTTAGTTGGCTCA	63665		-----	1452	Qy
Qy	1328	-----	1328		CAGCTCTTACCTGCATGTATGTCAAGCTTAGCCCTAGAGCACTGTCTCTTAACCTGGTCA	64797	Db
Db	63666	ATATTACAGATAGAGAACTGAGGCACAACTACTGCAGAATGGGGCCCGAGGAAGTGG	63725		-----	1452	Qy
Qy	1328	-----	1328		GCTTGATGGAAAGAGAAAGACAAACAGCCAGCAAGGGCGCTAGGGGGGTATCCC	64857	Db
Db	63726	GGGGTGTCTTCTGGTCTTGCATCATGATGGAATTTAGTTAGTTAGACACAGCC	63785		CTGAGCCAGGACACACTCAGTGTGGCCAGAATGATTCTAGAGAAATCTTTTGAANA	64917	Qy
Qy	1329	-----	1335		TTAGTGGCCACTCTTCTTTTGGGCCCGACACTTTAGAAAGCTAAGTCGGGAAGTTATAA	64977	Db
Db	63786	CTCCAGACACCATATGGTGACACCATGCTGTTCTCCCGAGGACTCATGGCCGGGCCA	63845		-----	1452	Qy
Qy	1335	leProProGluArgHisSerProHisLeuLysGluGlnHisIleArgGlySerI	1355		ATTTGAGGCTAACCTAGGCTACAAAGCTGTACTCTAGCTTAATGCCAGTACCACAGTTA	65037	Db
Db	63846	TC---CCTGAGCAGCAGACGCC---CACCTCAAGGAGCAGCATCACATCCGAGGCTCCA	63899		-----	1452	Qy
Qy	1355	leThrGlnGlyIle-----	1359		TAAAGTTTAATAACACACAGACATTGAGTAGCAATTGAGATCTAGGACCTAGCTGTGCT	65097	Db
Db	63900	TCACGCAAGGTAC-CTCCCTTATGGTGTGTGGTTCCCGCCCCCGGGCCCAAGTACAGCTAA	63958		-----	1452	Qy
Qy	1359	-----	1359		CCGTGTCGCCGTGGATCCCCCGCCCATCTCTCCATGATGTTCCTCAATAATTCCTCTCT	65157	Db
Db	63959	GGGGTTGGAACAGAGGGTGAGCTTCCCCACCCATGGTCTATAGGTGGAGTGAATACTTG	64018		-----	1452	Qy
Qy	1359	-----	1359		CTGTGGTGCCTCTGAGACCTTAACAGGGAATATGTAACTCCAGCTGGGACCGAGCCAC	65217	Db
Db	64019	GCCCCGACTCAAAGCTTCAGCAAGCAGCGCTTGTCTAGTGAATGGGAGGGGTCCAGATT	64078		AGCTGGCGTGGCAGCAAGTGCATCTGGCTATGGAAATTCATAGCATGTGAAGTGTGCA	65277	Db
Qy	1359	-----	1359		-----	1452	Qy
Db	64079	GAATGGAACTTTAGTCTGTCTGTGGTAAACTGAGCAGTGTGGTTTACTTAGCATC	64138		GTCCCCACTGGGTGAGGAAGGTTGTGTGACCTGAAAGTTAGCCTCACTCTGGAAACCCCTG	65337	Db
Qy	1359	-----	1359		-----	1452	Qy
Db	64139	CTCAGCGCATATGAAGAGACAGGCTTAGAAAAGTCAAGTTCGATGCCAGGGGCCACAG	64198		GGCCGGTGGTGACCCCTGGATGTGTAGCCAGACTCAAGTGAGCAGGGCGTCCAGCCTCTG	65397	Db
Qy	1359	-----	1359		-----	1452	Qy
Db	64199	GAAGGAAGGATTTGTGCTGACCTAGACCGGACCGGCAAGGCAGTGGACAGCCAGTGTCTG	64258		luAlaLysLeuLeuLysArgGluGlyThrProProProProSerArgAspLeuT	1394	Qy
Qy	1360	-----	1374		ProArgSerTyrValGluAlaGlnGluAspTyrLeuArgArg	1374	Qy
Db	64259	TGTGCTGACAGGCATCCCGAGGTCTTATGTGGAGGCGCAGGAGGACTACTTACGGCGGG	64318				

Db 65398 GACATCATGTCTGCTAAAGGTCTCTGTCCATTGTGCCAAGGGATTAGAGATGCCCCATC 65457
 QY 1452 ----- 1452
 Db 65458 CTGTGCAGACATACAGAAAGCGGCATCTGCCAGCCAAATACAGACCTGCACCTCTC 65517
 QY 1453 --GlnGlyThrProLeuLysTyrAspThrGlyAlaSerThrGlySerLysHisA 1472
 Db 65518 CCAGGGCACCCCACTCAAGTACGACTCTGGGGCACCTCCACTGCGACCAAGAAACAG 65577
 QY 1472 spValArgSerLeuIleGlySerProGlyArgThrPheProValHisProLeuAspV 1492
 Db 65578 ACGTGGCTCATCATCGGCAGCCCGCGGCGCTTTCCTGCGCCGCGCCCTGCGACCA 65637
 QY 1492 alMetAlaAspAlaArgAlaLeuGluArgAlaCysTyrGluGluSerLeuLysSerArgP 1512
 Db 65638 TAATGGCTGATGTCGCGGCGCACTGGAGGGTGGCTGCTATGAGAGAGTCTGAAGAGCCGGT 65697
 QY 1512 roGlyThrAlaSerSerGlyGlySerIleAlaArgGlyAlaProValIleValProG 1532
 Db 65698 CAGGACCCAGCAGTGTGTGTCAGGGGGCTCCATCACAGTGGGGCTCCAGTCTGTCGCTG 65757
 QY 1532 luLeuGlyLysProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaG 1552
 Db 65758 AACTGGGCAAGCCACCGCAAGCCACTGACTTACGAAAGACCAAGGGGACCCCTTCACCA 65817
 QY 1552 lyHisLeuProArgGlySerProValThrMetArgGluProThrProArgLeuGlnGlu- 1571
 Db 65818 GTCACCTGCCACGTGGCTCCCTGTGACCCAGGAGGAGCCAGCCACGCGCTTCAGAAAG 65877
 QY 1571 ----- 1571
 Db 65878 GTCAGTGGGTGAGACTCCCTCAGGCTGCCAGTGTGGGAGGGGAGCAGCTCACTTCCTAC 65937
 QY 1571 ----- 1571
 Db 65938 AGGATACCTGGCCACTGCTCTTGGCCACAGCCAGTGTCTCTGCTGCTGCTCTACAC 65997
 QY 1571 ----- 1571
 Db 65998 TGCATACAGGGCCCCCTGATAAAGTGTGTTTTTAAATATTCAGGCTGAGGAGAGGCTC 66057
 QY 1571 ----- 1571
 Db 66058 AGTAGCTGATAAGCATGAAGACAGAGTTCAAATCCCGACCCACCAATGAAGCCAGGCA 66117
 QY 1571 ----- 1571
 Db 66118 CACTCATGCACGTGTGTAATCTTATGCTTTCAGTGTGAGAGCGGAAAGCAAGCAGGAGA 66177
 QY 1571 ----- 1571
 Db 66178 GTCTCTAAAGTCTTGGGCCATAAGTGGAGTTAAATATCCAGACATGTGTGGAGGTG 66237
 QY 1571 ----- 1571
 Db 66238 AMAACTGACCTTCAAAATGTCTTGACTTCTCACTTACACACCATGGCACATTTCTCCATT 66297
 QY 1571 ----- 1571
 Db 66298 CATGTGCACACATACACACAGAAATAAAGTAAATCGTTCGAATGAACAGTTAT 66357
 QY 1571 ----- 1571
 Db 66358 CACTCCGTAGGCTTCACTGTCCAGTAGCACTGCTGCTGAAGCCCTGCTGTGAAGCT 66417
 QY 1571 ----- 1571
 Db 66418 CACCCCGAGTCTGTGTTCCCTCTCTGATTTCTTTTACCTCCCTGACTTCCACTCTCAT 66477
 QY 1571 ----- 1571
 Db 66478 CTCGATCCTTCTCAGCCTTTCCTGTGTGGGCCCTCTTTAGAGGGCTCCACCTTTGG 66537

QY 1571 ----- 1571
 Db 66538 TTCTGTTTATAGCAACCCCTGTATATACCCCAACACCCTAATTCAGATGTCCAGGCCAC 66597
 QY 1571 ----- 1571
 Db 66598 CAGGGAGGCTATGGCCAGTTCAGGCCACATCCTGGCTAGGCTTGTGTAGTGTGAT 66657
 QY 1571 ----- 1571
 Db 66658 CTGTGTTTGTATTCATTTCTCAGGGGCGCACTTCCCAACCATTTGAGATCATTTCTCTCT 66717
 QY 1571 ----- 1571
 Db 66718 CAAGCCTGTGTCTTCTACTTTTGTGTTTCATCTCCGACCTGGAGCAATGGCTCTTGG 66777
 QY 1571 ----- 1571
 Db 66778 GGCTCAGGGTTCTTGCCTGCTTTTGTCTTGGGGTGTCTCCAGCCCATGATAAAGTCAGACT 66837
 QY 1571 ----- 1571
 Db 66838 GGTGAGTGAATGCGGAATGTGTACAGGAGTAAATGATATTTTCCAGGGGACCAAC 66897
 QY 1571 ----- 1571
 Db 66898 AGCAGAGGGCAAGAGGCCCTGGGGTTTGTGACAGCTCAGCCTGTGTGGCCCCACTGAGGC 66957
 QY 1572 -----GlySerLeuSerSerSerLysAlaSerGlnAspA 1583
 Db 66958 TGAGGCTACTGTGACCTGTCCCAAGGCAGCTCTATCCAGCAAGCGTCCAGGACC 67017
 QY 1583 rGLYsLeuThrSerThrProArgGluIleAlaLysSerProHisSerThrValProGluH 1603
 Db 67018 GGAAGCTGACATCTACACCCCGGAGATCGCAAGTCCCAAGTCCCAAGCACTGTGCCGAGC 67077
 QY 1603 isHisProHisProLysProTyrGluHisLeuArgLysValSerGlyValAspL 1623
 Db 67078 ACCACCTCACCCATCTCCCTATGAGCACTTCTCCGGGGCTGACTGGTGTGGACC 67137
 QY 1623 euTyrArgSerHisIleProLeuAlaPheAspProThrSerIleProArgGlyIleProL 1643
 Db 67138 TGTACCGTGTGACATCCCATTTGGCTTTGACCCCACTCCATACCCGAGGATCCCTC 67197
 QY 1643 euAsp----- 1644
 Db 67198 TGAAGCAGGTGGGTGTCTGGGCCCTGTAGATTTGGGGCTTAATGATTCATCTCTCTGG 67257
 QY 1644 ----- 1644
 Db 67258 GTGGGCTCTTGGGGTCTGGAGAGTTGGGGCTAGGCTTAGTATAGAGATCATCCCTGGTT 67317
 QY 1644 ----- 1644
 Db 67318 AGCCAGGGCAGGTTCCAGGGTGGGCTTGGGATCCTGTCTCTCAGTGGGCTTCTTTTCC 67377
 QY 1644 ----- 1644
 Db 67378 TGGAGGATTCATCTGTACCTTGCAGTAAGTGAAGGGGCTCAAGTGAAGTGCATGACTTGAG 67437
 QY 1644 ----- 1644
 Db 67438 CCTTTTAAAGGCTCTTTTGTAGGGTGTCCAGGAGCTATATATTTTGACGATATATCTGT 67497
 QY 1644 ----- 1644
 Db 67498 GAGCACTTCCCAAGCATTCAGACAGACACCCCAATGATGAGGGAGCGAGTCTTAAGC 67557
 QY 1644 ----- 1644
 Db 67558 TCTGTGTGTACTGGGGAGGCATGTGGGTGCACAGGAGGAAGCTGAAGTGGGAGT 67617

Db 69745 GATGAAGGGGTAGATAGACATATGGGGCAGATGTTTTGGATGGATGGGTGGATGGAT 69804
 Qy 1898 ----- 1898
 Db 69805 GAGTTGGAGCAGATAGATAGTGTAGTGGATGGATATGTCCTGGTGGATGGATGGGT 69864
 Qy 1898 ----- 1898
 Db 69865 GAATTGGATAGTGGATATGTTGGACTGATGGACAGGTAAAGCAGACACACAGATGAATGGG 69924
 Qy 1898 ----- 1898
 Db 69925 TATACACTGGGCAGCTGGATGGTTGTGTATCACTGTGTAGATGATGATAGATGAATG 69984
 Qy 1898 ----- 1898
 Db 69985 TATAGAAAGGAAGATAGGGGTGGATGGATGGATGATGATGGATGGATGAGCAGA 70044
 Qy 1898 ----- 1898
 Db 70045 TGGTCCACGGATGGCTGGATGGACAGCAGATGAGTGGATAGCAGAGTGGGTGAATGAA 70104
 Qy 1898 ----- 1898
 Db 70105 TGGATGGAATAGAGTGGATGATGGGGTGGTGGATGGAGTCCGTTGGTAGTCATTA 70164
 Qy 1898 ----- 1898
 Db 70165 GTGTATAAGGCCAGAAATACAACTTCAGAGAACAGAACTGGGAGCTTAATGTGAGGCC 70224
 Qy 1898 ----- 1898
 Db 70225 GCAGGGCTGGTGTGCTCAAGGCGCTGGTGGCGGATGCTGCTGCTGAAGTCAG 70284
 Qy 1898 ----- 1898
 Db 70285 TCTCATGCTTCTGGCTCATGACCAACACACTGCTGAGAGGCTCCGCACTCCTGCCGACT 70344
 Qy 1898 ----- 1898
 Db 70345 TCTAGGCGTCTCTACTGGCCCTGCTGAGCCTCTGGCCCTCCCGCACCGGCTTCT 70404
 Qy 1898 ----- 1898
 Db 70405 TCTCTGACCTTGGGAGAGATAGTCTGCTCTGTCACTGTCTTCCAGAGCTCGGG 70464
 Qy 1898 ----- 1898
 Db 70465 CACCCTTGCTTAAGTGTGTATTCTGTATCATCTAGGAGGGTAAGAAGCTTTAGGTGATA 70524
 Qy 1898 ----- 1898
 Db 70525 GGGACTGAATAGAGCCGACACAGATAGAGGGTCACTCAGGAGGGCACTTGTCTGGG 70584
 Qy 1898 ----- 1898
 Db 70585 AGCCTCAGAGTGAATCTAGGAGGGACTCTCAGTCAGGACTCTGAAGGTGTGAGG 70644
 Qy 1899 ----- ArgSerThrSerTh 1903
 Db 70645 TAGGAAGCCATTGGCCAGCACTGCCCTGCTCTCTCCCTGTCTGCTGCAAGTCCACCTCCAC 70704
 Qy 1903 rSerSerProValArgProAlaAlaThrPheProAlaThrHisCysProLeuGlyGI 1923
 Db 70705 CTTCTTGGCTGTCCGCCAGCTGCCACATCCCACTGCCACCTGGCTGGTGG 70764
 Qy 1923 yThrLeuAspGlyValTyProThrLeuMetGluProValLeuLeuProLysGluAlaPr 1943
 Db 70765 CACCTTGAAGGGTCTACCTTACCCTCATGGAGCCGCTCTGTTACCCAGGAGACCTC 70824
 Qy 1943 oArgValAlaArgProGluArgProAlaAlaThrGlyHisAlaPheLeuAlaLysPr 1963
 Db 70825 TCGGGTGGCCCGGAGCGGCCCGGTGTGGACGCTGGCCATGCTTCTCTCACCACCAACC 70884

Qy 1963 oProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGluProArgPr 1983
 Db 70885 CCGGGCCCGG-----GAGCCCGCTCTCACCAGCAGAGAGCTCCGAGCCCGATC 70935
 Qy 1983 oLeuValProProValSerGlyHisAlaThrLeuAlaArgThrProAlaLysAsnLeuAl 2003
 Db 70936 CCTAGCACCCCGGAGCTCCAGCCACAGCATCGCCCGCAGCCAGCAAGAGCTTGC 70995
 Qy 2003 aProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAspProHisAr 2023
 Db 70996 ACCCCACCATGCCAGTCCGACCGCGCGG-----CCACCTCGGCTCAGATCTGACCG 71052
 Qy 2023 gGluLysThrGlnSerLysProPheSerIleGlnGluLeuLysArgSerLeu----- 2041
 Db 71053 AGAAAGAACTCAAAAGTAAACCTTTTCATCCAGGAATGGAACTCGTCTCTCTGGGTAA 71112
 Qy 2041 ----- 2041
 Db 71113 GACCACCTGACAGCGGCCAGCTTCATAGAGCAATAATCACGCGTCAAAATTGCTCAGGA 71172
 Qy 2041 ----- 2041
 Db 71173 AAGGGGGCGGAGAGAGGTTGCTGGCCACAGACTCCCTCGCGCAGCGTAAGACATC 71232
 Qy 2041 ----- 2041
 Db 71233 CGGCCCGCGCTGCCCCACCATCTGTGGCTAAAGATAATTTTCAGATCTTTGCTTTTA 71292
 Qy 2041 ----- 2041
 Db 71293 ATTTTTCCTCTTTTCGTTGGTTGGTATTTTGTTCGAGCTCGTCATCTCTGGTCAG 71352
 Qy 2041 ----- 2041
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 Qy 2041 ----- 2041
 Db 71413 ATGAGTTTTCCTCTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCT 71472
 Qy 2041 ----- 2041
 Db 71473 CTTTGTGGATTTTTCACCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 71532
 Qy 2041 ----- 2041
 Db 71533 GCGCCTCCCATCTCCCGCCACCACTGCACTTTCGTTTGGGGAGTGGGGATGCAAGGGG 71592
 Qy 2041 ----- 2041
 Db 71593 TACCAGTCACTGCTGCTACTGTTCTGGAGGAAGTCAAGGAGGAGCGAGGGGGGAG 71652
 Qy 2041 ----- 2041
 Db 71653 ACAGGTGGGGGGAGCTGGGTGCCACCTCTCTTCCACACAGCATATAAGGCCAA 71712
 Qy 2041 ----- 2041
 Db 71713 GCGAGTGATCAGGAGCAGTGGGCTGGGCAAGGAGGCGCTAGGAGACACAGTTGTCTAG 71772
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 Db 71773 GGACAGGTGTCACTCAGCTTGAACCCACACCATCACACCTTGACCCCATGCACACTCA 71832
 Qy 2041 ----- 2041
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 Qy 2041 ----- 2041
 Db 71893 CACACTGCCCAAGCCAGACTCCCAAGCTCCTTTGGGTGTCTGTATCTCTGTATCATATGGA 71952

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Db	71953	ACTGTCTGTCACTTGGCCATTCTCTTCTTGGCCCACTAGGCTTAGATAATTTCCCTTC	72012
Qy	2041	-----	2041
Db	72013	ATCTTGAGGCCCACTGTGTGAGGAATGGCTCATCCCAAGCACCCCAACCCCAAGCCC	72072
Qy	2042	-----GlyTyrHis---GlySerSerTyrSerP	2050
Db	72073	ACCCACCTCTTGACCCCGAGCTCACCTGTTTCAGGTTACCAAGTGAGGCTGGCTACAGCC	72132
Qy	2050	roGluGlyValGluProValSerProValSerProSerLeuThrHisAspLysGlyL	2070
Db	72133	CCGATGGGGTGGAGCCCATCAGCCCGGTGAGCTCCCGCAGCTCAGCCACGACAAAGGGGC	72192
Qy	2070	euProLysHisLeuGluLeuLeuAspLysSerHisLeuGluGlyGluLeuArgProLysG	2090
Db	72193	TCTCCAAACCTCTGGAAGAGCTAGAGAAGGCCACTTGGAAAGGGAGCTGCGGCACAAGC	72252
Qy	2090	lnPro-----	2091
Db	72253	AGCCAGGTAACACCCGGGAGAGTGGCAGGTGGGAGACTAAGGCACCGCTCCACGCTGTC	72312
Qy	2092	-----GlyProValLysLeuGlyGlyGluAla	2100
Db	72313	CCCAGGCCCTGACAAGCTCTGCTCGCTCTCTTAGGCCCCCATGAAGCTCAGCGCGAGGCT	72372
Qy	2101	AlaHisLeuProHisLeuArgProLeuProLeuSerGlnProSerSerSerProLeuLeu	2120
Db	72373	GCCATCTCCACATCTGCGGCCACTGCCGAGAGCCAGCCCTCATCCAGCCCACTCTCTC	72432
Qy	2121	GlnThrAlaProGlyValLysGlyHisGlnArgValValThrLeuAlaGlnHisIleSer	2140
Db	72433	CAGACTGCCCGAGCATCAAAAGTACACAGAGGGTGTGTCACCTTGGCTCAGCATCAG-	72491
Qy	2140	-----	2140
Db	72492	CGTAAGTGTCTATTTCTGGGCCCCCACCATTTGGGTGGATAGAGAGTGAGTCCCATAG	72551
Qy	2140	-----	2140
Db	72552	TCAGACAGATGCTAGCATGCATG6CCACTACACTCAGTCTGTGGCGGTGTCCACATA	72611
Qy	2140	-----	2140
Db	72612	AGGTCTGCTGGGACACTCACCCAGGAGACCAAGAGTCAGATCAGGGTCTGCGCTACT	72671
Qy	2141	-----GluValIleThrGlnAspTyrThr	2148
Db	72672	CTACACTGAAAGTCCTGACCTGCTCTCCCTCCACAGAGGAGTCAATACGAGGACTACACG	72731
Qy	2149	ArgHisHisProGlnGlnLeuSerAlaProLeuProAlaProLeuTyrSerPheProGly	2168
Db	72732	CGCCACACCCGCGACAGCTCAGTGGGCCCTCTCCCGCCCTCTCTACTCTCTTTCGCGGA	72791
Qy	2169	AlaSerCysProValLeuAspLeuArgProProSerAspLeuTyrLeuProProPro	2188
Db	72792	GCCAGCTGCTGCTCTGGATCTTTCGCGCCCAACCCAGTGACCTTACTCTCCACCCCCC	72851
Qy	2189	AspHisGlyAlaProAlaArgGlySerProHisSerGluGlyGlyLys-----	2204
Db	72852	GACCATGGCAACCCAGCCCGGGATCCCCCACAGTGAAGGGGGCAAAAGGTGAGGATAT	72911
Qy	2204	-----	2204
Db	72912	ACTCATATCTGTGTGATGCTTGGCTGAAGGATATTTGGGTAGGATCAGCTTGACTGTG	72971
Qy	2204	-----	2204
Db	72972	TTGGGCTAAATGGGAACCTGAGGCTCAGGGATACAGAAGTTCACTAAGCTCCAGAACCA	73031
Qy	2204	-----	2204
Db	73032	CACAAAGTCTAATCACGAAGGTGGCACACCCCAAGGCTCCATGTGCCAACTAGTGTCTCT	73091
Qy	2204	-----	2204
Db	73092	ATATATGCCAACTCAGCTAGGGTCTGATGTCCCATGCCCATTTAGCAGATAGGAAAAC	73151
Qy	2204	-----	2204
Db	73152	GAGSCATAGAGAAGTGTAGTTTACCATCCCATACCATGACACACATATTACCCCTGGCTGGC	73211
Qy	2204	-----	2204
Db	73212	CTGAGGCTCGGGCATGAGAGAAGCTGGGCCCTTACCTAGGCTTTAGGAGCGAGTGAAGC	73271
Qy	2204	-----	2204
Db	73272	ATCTTGTATGAGTTTGTATTTTAGAAGCACCGGTTACAGACAGTGAAGTTCTGGCATGGGTG	73331
Qy	2204	-----	2204
Db	73332	CCTCAGTGTGTGGSCACACACTCTACTCAGGTGAGATAGCTCTGCCAGGCTGAGGCAGG	73391
Qy	2204	-----	2204
Db	73392	AGGATTGTGAACCTTCAGGGCAGTCTGGGATGTACTGCAAGAACCCGACTCAAAATCAAC	73451
Qy	2204	-----	2204
Db	73452	AAAGCTTACAAGTCTTTTAGGTTATCTCAGAAGATCGTAGGCCACTGGGGTCTCCAT	73511
Qy	2204	-----	2204
Db	73512	ACCTCAGCTGCAGAGTGGCCATTTACAGGGAATGTGCAGGGCCCCGCTGTGGACAGTGG	73571
Qy	2205	-----ArgSer	2206
Db	73572	GGTCTCTCATCGGGTAGAACTTCACCTCAGCTAGGACGCTATCTCCATCAGGTCC	73631
Qy	2207	ProGluProAsnLysThrSerValLeuGlyGlyGluAspGlyIleGluProValSer	2226
Db	73632	CCAGAACCCAGCAAAACATCGTCTCGGCGAGCAGTGAAGTGCATTTGACGCTGTGTAT	73691
Qy	2227	ProProGluGlyMetThrGluProGlyHisSerArgSerAlaValTyrProLeuLeuTyr	2246
Db	73692	CCACAGAGGCGATGACTGAGCCAGGACATGCTCGGAGCGCTGTGTACCCACTCTGTAT	73751
Qy	2247	ArgAspGlyGluGlnThrGlu-----	2253
Db	73752	CGAGACGGGGAACAGGGCGAGCCAGGTAGCCACAGCAAAATCCGCGCTTAGAGATGGT	73811
Qy	2253	-----	2253
Db	73812	GGTGTGATGTTCCATGTATACCCCAAGGCTCGGCCCTCCCATATAGAGGCCCATTAATCCCT	73871
Qy	2253	-----	2253
Db	73872	CACAGCTCAGCGGGCTGATAGACCTTCAGGGGCCCTTCAGTTGCAGACCCCTGTCTGGC	73931
Qy	2253	-----	2253
Db	73932	ATCCTGTGCTGGCATCCCTGTGTCTGGGATCTCAGCCTGAGCCATGCCCTGTTTATC	73991
Qy	2253	-----	2253
Db	73992	ACTTGTGCTGTGATCTGGGAATGAACCTAAGTTGAACACAGACTGGGTGGGGTGGACATGGA	74051
Qy	2253	-----	2253
Db	74052	CTTCAGGGAGGGTGTGACCTGTCACCTGTCCAGTTCCCTGGGATTTCTTGTGTGATCTA	74111
Qy	2253	-----	2253

Db	74112	GCAATAGGCAATTGCTGGGGCAATTCACAGCGTACCTGGGATGGGAACCAAGCTGTCTCT	74171	QY	2322	-----	2322
QY	2253	-----	2253	Db	75251	GTTGTGGGGCTTGGGGCTGGGGCAGCTCACAAGTGTGACCTGAGGATTGGCCCTGG	75310
Db	74172	TAGCACTCAGGTAGCTCAAGTGTGAGTCCCTGTGCTAAAGTCAATGCCCCAGC	74231	QY	2322	-----	2322
QY	2254	-----	2265	Db	75311	GGTACAGAGATTGAGGGTGGCGCAGGCATCTTTACACTAAAGTCTCTGGCCATTTCTTA	75370
Db	74232	CTGCTGACCCGTGTCTCTGCTCCCGC-AGGATGGGCTCTAAGTCTCAGGCAACACC	74290	QY	2322	-----	2322
QY	2266	SerGlnProProAlaPheSerLysLeuThrGluSerAsnSerAlaMetValLysSer	2285	Db	75371	AATCAGATGCAGGCAGTAAATGTAGGGGAAAAGTGTCAAACTCACGTGCAGTTTGTGGCAG	75430
Db	74291	AGCCAGCCGCGAGCTCTTTCAGTAAGTCTGACTGAGAGCAACTCCGCCATGTGTAAGTCG	74350	QY	2322	-----	2322
QY	2286	LysGlnGluLeuLeuLeuLysLysLeuAsnThrHisAsnArgAsnGluProGluTyr---	2304	Db	75431	AAGTCTCAGGCTTTTCAGTATGTGTCTTGGGGCTTAGAGCATCCGCTTCCGCTGCTTAATTA	75490
Db	74351	AAGAAGCAGGAGATCAACAGAAACTCAACACCCACACCGGAACGAGCCAGAAATACAGT	74410	QY	2322	-----	2322
QY	2304	-----	2304	Db	75491	TCACGTTGGCCCTCGGAAAGAAAGCTTGTGCTGGGAACAAATGGGCTCGGTGACTGTGTG	75550
Db	74411	AAGGGAAAGCCAGGGCTAGAGCAGGCACCGGAGGGAGATAGTACTCTTAAACCTTACCA	74470	QY	2322	-----	2322
QY	2304	-----	2304	Db	75551	ACAGGGGAAGCTGTGAGGACTTAAATCCAGGCCAGAGGACAGGCAAGGTCCTACTTCC	75610
Db	74471	TGGAAGACCCAGTTCTGCCAGTTGGTACTAACTGACAAACAGCATATAGCACTTTGGT	74530	QY	2322	-----	2322
QY	2304	-----	2304	Db	75611	TTATTTGTGTGAGCCTTGGGCTTAGGGAATAAGGTGGCCAGATTAAACCTTTGGGACAT	75670
Db	74531	AATGCCCTGCACACAGTAGGTAGTCACAGGAAAGCTGTAGACAGCCCTGTGTGGGTGC	74590	QY	2322	-----	2322
QY	2304	-----	2304	Db	75671	TTCCAGAGACCAACAGGACCTGTAAAGGGATGGGGTAGGATCTCTGGCAGGACAGCCTG	75730
Db	74591	TGAGGACACAGCACACTACTCCAGGTTTCATGTGCAGACCCGGTGCTTTCACACGGC	74650	QY	2322	-----	2322
QY	2304	-----	2304	Db	75731	GGGCTTTCTGAGCCTCAAGCAGAGGAACTGACCGAGACAGGAACTGTGTGGAGAT	75790
Db	74651	TGATGGGTGGACAGGACTCATGTCTTACGCGAGGGTCACATGGGCCATATGCTTAC	74710	QY	2322	-----	2322
QY	2304	-----	2304	Db	75791	GCGTGTCTAGAGTGTCTAAATCTTGACATAGGTTCTAGACACCTGGGTGTATATGCA	75850
Db	74711	AAGAATGCACCGGAAAGCAACATGACAGCTTTGCACTGTCCCTCCCGAGGTGCCT	74770	QY	2322	-----	2322
QY	2304	-----	2304	Db	75851	TATAGATAGGTAAATACAGTGATTTGTGCTAAAACTAACTTAGTTGTCTCTCACACA	75910
Db	74771	GGACAGACAGCAAGTTCTTCTTCTGGAGTATAGAGCCCTCACAGGTAAACAGAGGC	74830	QY	2322	-----	2322
QY	2304	-----	2304	Db	75911	CACACACAGCATCCTCAACATCGCCCTTAAATGTTAGTTCTCAAAGACATGTTTCCA	75970
Db	74831	CTAAGTAGTGACCAACCGCTGAGTAAACCTGGAGCATCAGGTGCCTGTGTGCCAG	74890	QY	2322	-----	2322
QY	2304	-----	2304	Db	75971	GGCTAGCCAGTGACGTTCAACACCAACAAAGGTAGATGAGAGAAAAGTTATGGCTGT	76030
Db	74891	ACATTCAACTCAGACTGTACGGGGGACACAGAGGGGTGCAGATCTCTAGACCTGTGAG	74950	QY	2322	-----	2322
QY	2305	-----	2313	Db	76031	GCCAGTGCCATCAGGTCAACAGTCAACACCGAGACAGGCCAGGAGCCGTGCTC	76090
Db	74951	CTCAGCCTTCCACACCTTGTACCTGCTCTAGATATTGGCCAGCCTGGAGCGAAATC	75010	QY	2322	-----	2322
QY	2314	PheAsnMetProAlaIleThrGlyThr-----	2322	Db	76091	CATCAGGAAACTCCCTCTGTCCCTTTTCTGTGTACTCTCTCTCTCTCTCTCTCTTAT	76150
Db	75011	TTCAACATGCCCGGCATCACTGGAGCAGGTAAACCTCCTGTGTGTGCGCATGGCAAACTC	75070	QY	2322	-----	2322
QY	2322	-----	2322	Db	76151	TCTGGATGTAGAGAGTGGGTGGGGCTTGTATTTAAGGTTGAATTTGTGTGTGTG	76210
Db	75071	CCTTCCCGAGTGCTGACTTGGGGACAGGAGCCTTAGCCTCTCCCTGGTCTCAGTGGACC	75130	QY	2322	-----	2322
QY	2322	-----	2322	Db	76211	TGTGGCGCGGTGTGTGTGCGTGGCGCGGTGTGTGTGCGCATGCAATTCACCCCTGTT	76270
Db	75131	CAGATGACACAGATGGCAGCCTCCACTGCTAGGGTCTCTCCCTACATGAGGAGTGCCC	75190	QY	2322	-----	2322
QY	2322	-----	2322	Db	76271	GGAAGTTACGCTTTTCTTGGTAAACCTTTGCTTAGCACTGTGGGCACATGACCAACATGA	76330
Db	75191	AAGGTTGAGGTACAGGGTCCCTCAAGTGGGTGTAGGTACACCCCGGAAACACTTGGCCA	75250				

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QY 2397 ----- 2397
Db 78551 TAATCCTCTCACCTTCCCGCCCTCAAGCTTGGAGCCTGTGACCTTATTTTGTGCGTTT 78610
QY 2397 ----- 2397
Db 78611 GACATCTAGTTTCTAATCTAAAGCTGGTCTGACACCCCATGTTGGGAGGGCGCCGCC 78670
QY 2397 ----- 2397
Db 78671 CTTTTACCCCGACGACTGTCTGCTTTTCCGCTGCTCATCACTCCCCACATCTCCCTCG 78730
QY 2397 ----- 2397
Db 78731 CTGTGTGACAGGATGACAGCGCGCAGCGCCAGGCCACCACTACTGTGTGGCCAGGGCCTCTGGGAA 78790
QY 2397 ----- 2397
Db 78791 GAGTCTAGTGTGGCGGTGACCCCTTGAAGCCAGACAGCACAGCTCCCCACTCTTCCAAT 78850
QY 2397 ----- 2397
Db 78851 GTCCGTCAGCACTTGTGTTTCCAAGCAGACACAAAGCAAGAGGTGCCCTGCTGTCCC 78910
QY 2397 ----- 2397
Db 78911 CTTCTAGGGTCAGGCCAGCCCCCGGTCTGGCGCTCTACGACAGAGCCTTCACTCCGGCATA 78970
QY 2397 ----- 2397
Db 78971 GTTGAGTGTCTCTTGGGCAATGCTGTATCCAGCCAGCAAGATCTGACATTCCTCAGTGAG 79030
QY 2397 ----- 2397
Db 79031 GGGTACAGTCTGTGGGAGCACCTAAGGAATAGTCAATCTCTCTCATAGTAATG 79090
QY 2397 ----- 2397
Db 79091 TTCAATGCTTTCTTACACACAGGGCTGGCTCTGGCCATCTGGTAGACCTCTTAGCCCTCC 79150
QY 2397 ----- 2397
Db 79151 TGGCTCAGGTTTCTCACACTAGTGTCTGTCTGGGGCCCTAGGAGCAGGTGGCTCC 79210
QY 2397 ----- 2397
Db 79211 CCAAGGCAGAAATCAGCCCCCACTGCCCTCTCAGTGTGGTGGGTGCTTACTGTCAA 79270
QY 2398 ----- GlyGlyGlyLysAlaLys 2404
Db 79271 CCCCGTCTGACTTGGCCCCCTTCCACTTTGTCCTCGAGTGGAGTGGGAAAGCCAAG 79330
QY 2405 ValSerGlyArgProSerSerArgLysAlaLysSerProAlaProGlyLeuAlaSerGly 2424
Db 79331 GTCTCTGACAGACCTAGCAGCGCGAAAGCCAAAGTCGCCAGCAGCCAGGCGCTAGCGTCCGGA 79390
QY 2425 AspArgProProSerValSerSerValHisSerGluGlyAspCysAsnArgAlaThrPro 2444
Db 79391 GACCGACCCCTCTCTCTCTCAGTCACTCAGAGGGGAGTCAATTCGCCGGAACCA 79450
QY 2445 LeuThrAsnArgValTrrpGluAspArgProSerSer----- 2456
Db 79451 CTCACCAACCGTGTGTGGAGGACCGGCCCTCACTTCGAGGTGGGTATCAGTAGGAGTA 79510
QY 2456 ----- 2456
Db 79511 GAGATGTATCCAGGGTTGGGGTTTACCTGGGCTACCCAGAAAGAGTCCCTGTATCAC 79570
QY 2456 ----- 2456
Db 79571 CACTTAGCAAGAGGATATAGAAAGAAACCTATCAGAGGGTCTGTGTAGTGGCCAGAC 79630

QY 2456 ----- 2456
Db 79631 CTTCCAGGCATGGCTCGTGCATACAGGGGAGGCTGCGAGCCCTTTCTTGGCTGTGAGGCACT 79690
QY 2456 ----- 2456
Db 79691 CTAGGATTTTGACAGGACAGTAAGGCAGTAGAAGACAGGACAGAGGGAGAGCGGAAAGG 79750
QY 2456 ----- 2456
Db 79751 TTTTACTGAGTCCAGTCAATATGGTGTAGGCTGTGCGACACAGGACAAAGGGAGGAG 79810
QY 2456 ----- 2456
Db 79811 GCCGGTTTGAAGAACTCCAGAGTTAGAGGTCTTGCCCAAGAGAGACCCAGGCTCTGGTTT 79870
QY 2456 ----- 2456
Db 79871 CTTATATGAAGACGGGTCTGAGTGTGCTACGTAGGGCTTGCAGAGCCTCTGCGAG 79930
QY 2457 ----- AlaGlySerThrProPheProTyrAsnProLeuIleMetArg 2470
Db 79931 CACTCTCCATCTTCTCGCAGGGTCCAGGCCATTCCCTACACCTTTGATTATGAGG 79990
QY 2471 LeuGlnAlaGlyValMetAlaSerProProProGlyLeuProAlaGlySerGlyPro 2490
Db 79991 CTACAGGCAGGTGTCTATGGCTCTCCCGCCCCCACCCTTGGCGCAGGCGCGGCC 80050
QY 2491 LeuAlaGlyProHisAlaTrpAspGluProLysProLeuLeuCysSerGlnTyr 2510
Db 80051 CTAGCTGGTCCCCCACACCGCTGGGATGAGGAGCCCAAGCCACTGCTGTGTTTCAAGTAT 80110
QY 2511 GluThrLeuSerAspSerGlu 2517
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RESULT 14
US-10-087-192-652
; Sequence 652, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 233380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(233380)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-652

Alignment Scores:
Pred. No.: 3,26e-168 Length: 233380
Score: 2951.00 Matches: 1381
Percent Similarity: 17.11% Conservative: 58
Best Local Similarity: 16.42% Mismatches: 238
Query Match: 22.33% Indels: 6744
DB: 12 Gaps: 54

US-09-522-753-5 (1-2517) x US-10-087-192-652 (1-233380)

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Qy	765	AsnGlyProLysProProAlaThrLeuGlyAlaAspGlyProProGlyProProThr	784	
Db	197510	AGTCCCTCGCCCACTGTGTCCAGGCTCTGTGTGGAGAGCCCACTCTCTCTCTCT	...	197569
Qy	784	-----	-----	784
Db	197570	CTAGGCTCTGGGTTCCAGAACGAGGAGACCTGCCAGGAGGTTAAAGGAATCGAGTG	-----	197629
Qy	785	ProProArgArgThrSerArgAlaProIle-GluPro	-----	796
Db	197630	CCGGGAAGAGAAATTCCTGGCAGCTTAGGGCACCAGGGGTGTGGAGATGAAGCTGCT	-----	197689
Qy	797	-----ThrProAlaSerGluAlaThrGlyAlaProThrProPro-ProA	811	
Db	197690	AATGGGCGCTCTCTCAGCACTGCAGCTCGAGGCGCGGAATTGCTCTCTCTCCATCCAC	-----	197749
Qy	811	laProProSerProSerAlaProProProValProLysGluGluLysGluGluLut	831	
Db	197750	TTCGGCTGTGGCCGAGCCCTCCCGAGGCTG-----G	197785	
Qy	831	hrAlaAlaAlaProProValGluGluGluGluGluGluGluGluGluGluL	851	
Db	197786	GAGTGGAGTGGCCCGGTG-GCTTAGAACATAATGCACTCTCTCTGCCACAGAGA	197844	
Qy	851	euAlaValAspThrGlyLysAlaGluGluProValLysSerGlu-CysThrGluGluAla	870	
Db	197845	TAGCCTGGAGACAGC-----CTGCAGCTGTCTTGGGTGCC	197883	
Qy	871	GluGluGlyProAlaLysGlyLysAspAlaGluAlaAlaGluAlaThrAlaGluGlyAla	890	
Db	197884	AGCTCATGCCCTGGT-----GCCCTGGACCGAGTCCCTGGGGGTG	197925	
Qy	891	LeuLysAlaGluLysLysGluGlyLysGlySerGly-----ArgAlaThrAlaLysSer	908	
Db	197926	CGCGGAAGCTGGGAAGGCTGTGTGTGG-GGTAGTCAAGAGCTTGTCTTGAGAGTCA	197984	
Qy	909	SerGly-----AlaProGlnAspSerAspSerAla	919	
Db	197985	CTGGGTAGAGTCCCACTTGGGACCC-CAGACCACTGCTGAGCCTTTATAGGCCCTTCAG	198043	
Qy	920	-----ThrCysSerAlaAsp	924	
Db	198044	CGTATCGTCTTCATCATGGTTTCAGTCGGGGCCCTTTAAACTCTCGTCTCTCTCGGCG	198103	
Qy	925	GluValAspGluAlaGluGlyLysLysAsnArgLeuLeuSerProArgPro	942	
Db	198104	CAGTAGGCACTGACGGCAGCGCAGGTGTAGACTGTAGGAGTGGGAGGACTGTAGG	198163	
Qy	943	-----SerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSer	956	
Db	198164	GAATGGGAGGAGTGTGTGCTGCTCAGCGCTCCAC-TCCCTCTGGCCACCGGTTCAG	198222	
Qy	957	Pro-----	957	
Db	198223	CCAGGTTTCTCATCTCCGTTTCTATCTGAATCTCCCGATGTTTAAACATCGGCGATTAA	198282	
Qy	958	-----GlnLysProLeuAspLeuLysGlnLeuLysGlnArgAlaAla	971	
Db	198283	TTTGGAAAGTTTCTGAACAGCAACCTAGTACCTCTCTGTGGCAACCCCTGGAGTAGCT	198342	
Qy	972	AlaIleProProIleGlnValThr-----LysValHisGluPro	984	
Db	198343	CACGGCCGTGGGCCACACAGCAATGTTGAAGCCCGAGAGCCTGTGATGTGCTCA	198402	
Qy	984	-----	984	
Db	198403	TTCCTCTCAGGGGTGGGGGGGTCTCCGGGGCTCATTTCTGATAGCTCTGGACTCGG	198462	

Qy	1263	LeuPro-----LysGlyHisValIleTyrGluGlyLysGlyHisVal	1277	Db	200418	GATCTAGCTCACTGAGCCTCCGCTTTTACGGCTTAAACAATCTCCACATCTCAGCCTC	200477
Db	199351	CTGCCTGTCTGCTGCCACCGCTGT-----CCTGGCC-CGTGCCACGCTC	199397	Qy	1356	-----	1356
Qy	1278	LeuSer-----TyrGluGlyGlyMetSerValThrGlnCysSerLysGlu	1292	Db	200478	CCAAGTAGCTGGGACCACAGATGCACACCACACATCTAGCTAAATTTTGTATTTTGTGA	200537
Db	199398	CTACCGAGTGCCTTGTGTGTTTCCAGGTGGCATGTCTGTGACCCAGTGTCTCCAGGAG	199457	Qy	1356	-----	1356
Qy	1293	AspGlyArgSerSerGlyProProHisGluThrAlaAlaProLysArgThrTyrAsp	1312	Db	200538	GAGTGGGTTTACCAATGTTGCCAGGTGGTCTCGAACTCTGAGCTCAAGCTGTCTG	200597
Db	199458	GACGCAAGACAGCTCAGACCCGCCCATGACACGCGCCGCCAAGCGCACCTATGAC	199517	Qy	1356	-----	1356
Qy	1313	MetMetGluGlyArgValGlyArgAlaIleSerSerAlaSerIleGlu	1328	Db	200598	CTGCCGACGCCCCCAGAGTGTGTGGATTTACAGCGGTGAGTACTGCACCCAGCCTGTG	200657
Db	199518	ATGATGAGGCGCGTGGGAGAGCCATCTCTCAGCCAGCATCGAAGGTGATAGCAGG	199577	Qy	1356	-----	1356
Qy	1328	-----	1328	Db	200658	GTTTTAGCTTCATGATTTTCATAGTGTTCCTCGATTTGTGTGAGGTGTTTCAGTTAATATCT	200717
Db	199578	GAGGAGACTTCATCTCTCGGTGCCCTCGTGGGCGGTGGGGGATGGCTGACCCCGTTT	199637	Qy	1356	-----	1356
Qy	1328	-----	1328	Db	200718	TGTTTATGTGTGAAGAAGCTGAGGCCAGAGAGGTTCAGATTTCTTGGTCAAGGTACAC	200777
Db	199638	TACAGATGGGAAACCGAGGCTGGGCTTTCTGAGGCTCCATCTGAGGTAGCCAGGGAC	199697	Qy	1356	-----	1356
Qy	1328	-----	1328	Db	200778	AGCAAGTGGGATTTGAACTCAGGCAGACTAGCTCCAGAACCCACTGGTGTGGAGGCTCT	200837
Db	199698	CTTCCCGTGGGTCTTACTTCCACCATCTGTTGGGATGACCACTGGCGGTGTAAAC	199757	Qy	1357	-----GlnGlyIlePr	1360
Qy	1328	-----	1328	Db	200838	TGATCGGTCTGGTGGGCGGGCGTGGGTGAGGTTCAGTGTCTCGGCCGCGCAGGGATC-CC	200896
Db	199758	ACTGACCCCTGTACTGCCAGTGTGGCTCAGGAGCCACGNAATGATGGCTCACCCCT	199817	Qy	1360	oArgSerTyrValGluAlaGlnGluAspTyrLeuArgArgGluAlaLysLeuLeuLysArg	1380
Qy	1329	-----GlyLeuMetGlyArgAlaIleProProGluArgHisSerProHisHisLe	1345	Db	200897	TCGGTCTTACGTGGAGGCACAGAGACTACTCTGCTCGGAGGCCAAGCTCTTAAAGCG	200956
Db	199818	CTCCTACCGAGTCTCATGGGCGGTGCCATCCGCGGAGCGACACAGCCGCCACCACT	199877	Qy	1380	gGluGlyThrProProProProProSerArgAspLeuThrGluAlaTyrLysThrG1	1400
Qy	1345	uLysGluGlnHisHisIleArgGlySerIleThr-----	1356	Db	200957	GGAGGACAGCTCTCGCCCCCACCCTTCAGGACCTGACCGAGGCTACCGAGGCTACAGACGA	201016
Db	199878	CAAGAGCAGCACCATCCGCGGTTCATCACAAAGTACTGCCCTGTCTCCATCGAC	199937	Qy	1400	nAlaLeuGlyProLeuLysLeuLysProAlaHisGluGlyLeuValAlaThrValLysG1	1420
Qy	1356	-----	1356	Db	201017	GGCCCTGGGCCCCCTGAGCTGAAGCCGCCCATGAGGCTGTGTGGCCACGGTGAAGGA	201076
Db	199938	CTCGTGGCCCCAACGGGTGTACGTACGACGAGGCGGGGAGGAGACACAGCCAGA	199997	Qy	1420	uAlaGlyArgSerIleHisGluIleProArgGluLeuArgHisThrProGluLeuPr	1440
Qy	1356	-----	1356	Db	201077	GGCGGCGCGCTCCATCCATGATCCCGCGCAGAGCTGCGGCACACGCCCGAGCTGCC	201136
Db	199998	GTGTGTGGGAACTCAGGACAAAGTATGCAGAAAGCCTGCAGCACACATGTACATGATCA	200057	Qy	1440	oLeuAlaProArgProLeuLysGluGlySerIleThr-----	1452
Qy	1356	-----	1356	Db	201137	CTTGGCGCGCGCCCTCAAGGAGGGCTCCATCAGCGAGGTATGGCCCGGCGCAGGCA	201196
Db	200058	GTACGTGAGCTACGAGCAAGGTGTCTCTTACTTATTTCAAAACAAAACAAAAGCAA	200117	Qy	1452	-----	1452
Qy	1356	-----	1356	Db	201197	CACGGGCCAGTTCTTAGGAGGTGGCGTGTGGGGCACTGCCCTGGGCTCTCCA	201256
Db	200118	AATACACCGATCACCCCTGTGCTTTTAGTGTGCATAGCAACTGTCTGTGTGGCA	200177	Qy	1452	-----	1452
Qy	1356	-----	1356	Db	201257	CATGGGAAACCGAGGCTGAGACCCCTCGGTACCTTACAGTCAACCAGCTGTCTATCAC	201316
Db	200178	CTAACCCAGGTGCCACCTCGGTATCGTTTTTACAGAACATCTTGTGGGACATCGGATT	200237	Qy	1452	-----	1452
Qy	1356	-----	1356	Db	201317	CGGCGCTCAGCTGTGCTGTTCCAGGCTGCGCAGGGGCAACGAGCTCTGTGACCTGATT	201376
Db	200238	GGGAGAGGTTGGAGAGCTCCGAGAACTCTTTTACAGTCTTCGCGGTGTTCCATGGCACA	200297	Qy	1452	-----	1452
Qy	1356	-----	1356	Db	201377	CTACTGAACCTACATGTTTCCCATTTCTTACGAGGAGGAACTGAGTCCCGAGAGGCCAG	201436
Db	200298	GCCAGTACTGTGAACCTGGCAGCTTTGTGGGTTTATTTTATTTTATTTTATTTTGTG	200357	Qy	1452	-----	1452
Qy	1356	-----	1356	Db	201437	GCAGCTTCCAGGCCACAGGACTAAACATAGTACGAGTAACTGCTCCGTTGAACTCT	201496
Db	200358	TTGTTGTGCTTTTGGACAGGGTCTATTCTGTGGCCAGGCTGGAGTGCAGTGGCAC	200417	Qy	1452	-----	1452
Qy	1356	-----	1356				

Db	201497	TGTGAGGGTCCAGGTGCGGCTGAGGATGTTGGCATGCGTTCAITGTTTACCCCTAGCA	201556	Qy	1452	-----	1452
Qy	1452	-----	1452	Db	202637	GTTAGCAAGCCCTCTGTCTCCCTGCTCTGGAGGCATCAGATGCTCACTTCCATCTTATA	202696
Db	201557	ATGCTCTGAGGTGTTTTCTTAATGACTTATTTATTGCTGAGTAAATTGAGTTTCAGA	201616	Qy	1452	-----	1452
Qy	1452	-----	1452	Db	202697	GATGACAACTTTTGTAGGCTCAGAAAGGGGATGCACTGGTCTGGGCTATGGCTGTGGC	202756
Db	201617	GAGGTTCAACGACTCACCCAGAGTCACGCAGAAATGCAAGTTGTGAAACCAATTCAGA	201676	Qy	1453	-----	1463
Qy	1452	-----	1452	Db	202757	CAGGGCTAGAGCTTACATCCCTCTGCCCGCAGGACCCCGCTCAAGTACGACACCGGCG	202816
Db	201677	TGTTCTACAGCCGACGATCCACTGCACCCACAGCAGGTTGCACCAAGAGGCCCA	201736	Qy	1463	-----	1483
Qy	1452	-----	1452	Db	202817	CGTCCACCACTGGCTCAAAAAGCAGCAGCTAGCTCCCTCATCGGACGCGCGCGCGA	202876
Db	201737	GTCCCCCAGCGGSCCCAGCTCAGTAGGGGAAGTTCCGTGCCGATGTTACGAGGACGAG	201796	Qy	1483	-----	1503
Qy	1452	-----	1452	Db	202877	CGTTCACCCCGTGCAACCCGCTGGATGTGATGCGCGACGCGCGGCACTGGAACGTGCCT	202936
Db	201797	GAGCTGTTCCGTGGAAAGCCCCCTGAAGGCCACTGTCTTCCACATGGGCAGAGTGGCCT	201856	Qy	1503	-----	1523
Qy	1452	-----	1452	Db	202937	GCTACGAGGAGAGCTGAAGCCGCGCAGGACCGCCAGAGCTCGGGGCGCTCCATTG	202996
Db	201857	CTTGTGAAGGGGAAGGAGAATGGAGCCACACGCGGCTGTGGGCTGTGAGGCGGAAGG	201916	Qy	1523	-----	1543
Qy	1452	-----	1452	Db	202997	CGCGCGCGCCCGGTCATTGTGCTGAGCTGGGCAAGCCGCGCAGAGCCCCCTAACCT	203056
Db	201917	ACTGGGTGGGTGTCGCGGAGGGGTTCCAGCTTGTAGGAAGTTTGAAGCCAGGAGA	201976	Qy	1543	-----	1563
Qy	1452	-----	1452	Db	203057	ATGAGGACCAACGCGGACCCCTTTGCGGCGCACCTCCACAGAGTTTCGCGCGTGCACACG	203116
Db	201977	AGGCAGAAAGCAGTAAGATCCCTGATTCAGGGAAGGTTTGGCTCTCAGCCCTTAGGC	202036	Qy	1563	-----	1571
Qy	1452	-----	1452	Db	203117	GGAGGCCACCGCCGCTCGAGAGGGTGAGTGGGTGTGCATGGCGGTGAGTGGGGTG	203176
Db	202037	AATTATGGAGTCTTGTGAAGCATCCACCGCATGACCAAGACAGGGTCCAGATTCTAGAAT	202096	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203177	GGCGCTGTCTGGAAGTGTGCTCCCATCCACATTAGCTTAGTTTGCACCTGGGA	203236
Db	202097	ATTCTTTTGAACAAGGCGAGTTCCCTTCTTACGACAGTAATGAAGACATCCCTAAA	202156	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203237	TATCTCGCCACCGCTTTCCACCATCAAAACACCTGCAGGCGCGTGGGCTCTGCCT	203296
Db	202157	TAGAGTTTGTGTTGTCGAAAGCCCTAAAGTCCACCATATCAAGTGTCTCCGAAGCCTG	202216	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203297	CCGATTCCAAAACCTGTCCAATCTCTTGCCACCTCCAGACACCGGTGTCTCACCTA	203356
Db	202217	CTGAAAAGAGCAGGGGACCTGTGGCTGGCTACGAAGGTCCAGTCTGGACTGTGACC	202276	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203357	GCTTCCCCCAGGCCCCCTCTCTCTGCTGTAATCCACTCTGCAACAGCTACCCGAT	203416
Db	202277	CCCCCATTTCTCACCATCTTCTGTCTGAGGGGCAACACCTCAGCCCTGACCTCAGT	202336	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203417	ACTTCTAAAAATGCAAAATCATATTATTCACCTTCCCTGCTTTTCATCTTCTAGCAACTT	203476
Db	202337	GTCCCTGGGCTGAAAGCCTCAGGGCGGTAGTATTGGGTCTGGGTGCTGACTTTTTCGTG	202396	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203477	CACACATTTTGTATGGCTTTGGGGGCGCTGCCTGTGTTGGGGCCCTGCCTGCCTCTCATTC	203536
Db	202397	CTTGGCATTTGGTGGGCCATGGAGGGTCCAGGCTGAACAGAGGAATGTTTTTTTACCCAC	202456	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203537	AGCGGATTCCTTGTCTCTCCCGAGCCCGAGCCCTGGGCGCTTTCTCTTTGTTCCCT	203596
Db	202457	ATGAGGTTGTTGGCTTCTTCTCGAAACTCCAGGGAACCATCAGAGAGCCCACTCG	202516	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203597	GGCATGCTTAGCTCGGTCAAATTCAGTCTTTGTGGGGGCTTTGCGTGGCTCTCTCTCT	203656
Db	202517	CGGAGGAGAGTTGACTGTGAACTTTTACCCCTTCTGCACTCCCGGAGGAGCGT	202576	Qy	1571	-----	1571
Qy	1452	-----	1452	Db	203657	CTGCCTGCCATGTCGCGGCTTCAGATCTTTTACTTAGTGGGTTTCTTTCCATCCCTCAG	203716
Db	202577	GGGACCAAGGTCAGGCGCCAGGGTGCAGGGCAGTAAGTAACAAGTGTGCCATCTCAGG	202636				

QY	1571	-----	1571	Db	204797	TGTTTCGCTCAGGACTCCTTAGGCATCAACTGTCAGGTTCCCTCGATGCGCAAACTGAG	204856
Db	203717	GTCTTTGTTTACATATTACATCCTTGGGAGGCTTCTTAACAGACCCCTATCTCCAGTT	203776	QY	1644	-----	1644
QY	1571	-----	1571	Db	204857	GCCTCGGGATTGGAAGACCCACACAGTGTATCATGAGCTTAGTTGGAGCAGAAATTTCTC	204916
Db	203777	CATATCACATGCTGTGACATTTTAAAAATTTGTTCTTCGGCCAGGCATGGTGGCTCACCT	203836	QY	1644	-----	1644
QY	1571	-----	1571	Db	204917	TTAGTAGTTTCAGGACATGTGGGTTAAACAATTCAGTGGTTTCTTTTCCGCGCAGGAC	204976
Db	203837	GTAATCCAGCAGTTTGGGAGGTCAAGGCAGGCAGATCACCTGAGGTGAGGAGTTCAAGA	203896	QY	1644	-----	1644
QY	1571	-----	1571	Db	204977	TTATCAGTGCCTTTAGCAATGCAAGGTATAGAATGAGGACTTGAATATATGCAATTTTTC	205036
Db	203897	CCAGCTGGTCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAATAACCGGT	203956	QY	1644	-----	1644
QY	1571	-----	1571	Db	205037	AAATAGACATGATCTGAAAGCTCTTTTAAAGTTGCCGGCAGGTGGCTCACACCTGT	205096
Db	203957	GTGGTGTAGCCACCTGTATTCCAGCTACTCGGGAGGTGAGGCAGGAGATCACTTGA	204016	QY	1644	-----	1644
QY	1571	-----	1571	Db	205097	AATCCAGCCTTTGGGAGGCCGAGGCGGATCACAGGTGAGGAGATGAGACCAT	205156
Db	204017	GCCTGGAGGAGAGGTTACAGTGAACGAGATCGTGCCATTGCACTCCAGCCTGGGCAA	204076	QY	1644	-----	1644
QY	1571	-----	1571	Db	205157	CCTGGCTAACACGGTGAAACCCCTCTACTATAAAATACAAAACTAGCCGGGTGGT	205216
Db	204077	CAAGAGTGAACTCTTATCTCAAAAAAATAAAGAAATTTTCTTCTGAGCGTG	204136	QY	1644	-----	1644
QY	1571	-----	1571	Db	205217	GGCGGGCGCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGATGGCGTGAACCG	205276
Db	204137	TTTCACTCTGTAATCTCATTTGTTGCTAGTTTATCACCTGTCTCTCGCATTAATGTC	204196	QY	1644	-----	1644
QY	1571	-----	1571	Db	205277	GGAGCGGAGCTTGAGTGCAGTGAGCCAAAGATCGGCCACTGCCTCCAGCCTGGCGGACAG	205336
Db	204197	AGCTTGTGAGGCTGGGATTTCTGTTCATTCACTGGGGTGACCCAGTTCTCACACAA	204256	QY	1644	-----	1644
QY	1571	-----	1571	Db	205337	CGAGACTCCTTCTCTAAAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA	205396
Db	204257	TGCTTCCACGCTAGTAGGCTGCATCAATATTTTAAATGATGAGTGAATGGA	204316	QY	1644	-----	1644
QY	1571	-----	1571	Db	205397	CCTTTGGAGTGTAAATCTGCAATGGGATGTCCTATGTTTGGGACAACTTTGATGCAAAA	205456
Db	204317	TGAAGAATGAATTTTAAAAAATAACACAAAAAGCAATGAGTCAGTGAGCAAAAAG	204376	QY	1644	-----	1644
QY	1571	-----	1571	Db	205457	GCATCCTTCGTAGAAAGTCAACCTCTTGTCTCTGGGTGATGTTTCTGTCTCGCAGC	205516
Db	204377	TGAACCTAAGCAATGAAGAAATGAAGAGTGAATGAAGAGACCTGCTCCTTGGGATCCG	204436	QY	1644	-----	1644
QY	1571	-----	1571	Db	205517	CTCAGTTCTGGTTTGTGCTTTGGGCGAGCCACACATGTAGGTGGGAGAGCTGTCCGGGTG	205576
Db	204437	AGGTCCCTATCTCAAACTCCCGGTAAATGCCAGGCCCGGATGCATCCAC	204496	QY	1644	-----	1644
QY	1572	-----	1587	Db	205577	CAGAGTAGGGGCGATCCAGACAGGTGGAGCGACCATCAGGCCTAGGTATGGCTGGCC	205636
Db	204497	CTTGCCCGTCCACAGGACGCTTTCGTCCAGCAGGCATCCAGGACCGAAAGTGCAGT	204556	QY	1645	-----	1657
QY	1587	erThrProArgGluIleAlaLysSerProHisSerThrValProGluHisProHisP	1607	Db	205637	TCACATGAGTCCCTCTGTCGCCCGAGCGCTGCTACTACCTGCCCCGACACCTGGCC	205696
Db	204557	CGACGCTCTGTGAGATCGCAAGTCCCGCACAGCACCGTCCCGGAGCACCCACAC	204616	QY	1657	roAsnProThrTyrProHisLeuTyrProProTyrLeuIleArgGlyTyrProAspThrA	1677
QY	1607	roIleSerProTyrGluHisLeuLeuArgGlyValSerGlyValAspLeuTyrArgSerH	1627	Db	205697	CCAAACCCACCTACCCGACCTGTACCCACCTACCTATCCCGGCTACCCCGACACGG	205756
Db	204617	CCATCTCGCCCTATGACACCTGCTTCGGGGGTGAGTGGCGTGGACCTGTATCGCAGCC	204676	QY	1677	laAlaLeuGluAsnArgGlnThrIleIleAsnAspTyrIleThrSerGlnGlnMetHisH	1697
QY	1627	istIleProLeuAlaPheAspProThrSerIleProArgGlyIleProLeuAsp	1644	Db	205757	CGGCGCTGGAGAACCGGCAGACCATCATCAATGACTACATCACCTGCAGCAGATGCACC	205816
Db	204677	ACATCCCTGTGGCTTCGACCCACCTCCATACCCCGCGCATCTCTCTGGACGAGGTG	204736	QY	1697	isAsnThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeuSerProArgG	1717
QY	1644	-----	1644	Db	205817	ACAACGGGGCCACCGCATGSCCAGCGAGCTGATATGCTGAGGGGCGCTCTCCGCCCGCG	205876
Db	204737	ATTGCCCTGGGCTCCAGAAACCTGCAGTGGTGTGACAGGGCCACGACCTCATCAG	204796	QY	1717	luSerSerLeuAlaLeuAsnTyrAlaAlaGlyProArg	1729
QY	1644	-----	1644				

[illegible]

Db	214635	GAACAGACGAGGCCAG-GTACTTCTGTGGGCACATGGCTGCCCCCGGGATGCTCTGGT	214693
Qy	2255	-----	2255
Db	214694	ATCCCTTGCCCATCTTTGGCCCCCAGTCCACCGTGGTGCCATGTGGAGAGTGACAAGGGCA	214753
Qy	2255	-----	2255
Db	214754	CAGGGCTCAGTGGTGACCTCAAGCCTGCGCAAGCAGGTTTACCAACTTTGGGGGTGTGA	214813
Qy	2255	-----	2255
Db	214814	TACATGCCACCCCTCCCTGGGGAGACCTCAGTGGTAGCTTTTCCATGTCTTTGGGGTGGGAT	214873
Qy	2255	-----	2255
Db	214874	CTCAGCTGGACAGGCCCGGTTGACAGCCCTGTTGAACCTCTAAGAAATAATGACTA	214933
Qy	2255	-----	2255
Db	214934	GGTGTGTCGGCCAGACCGGGGCGATGGGTGAGGTGGGACCTCAGAAGGAAGCTGGGCC	214993
Qy	2255	-----	2255
Db	214994	CGTGCCCTGGGGAAGGCATGATCGGAACCCAAATTTCACTGCTCTGGGGCTCTTTGAG	215053
Qy	2255	-----	2255
Db	215054	AGSGTCAGGCTGGAGCAAGTGGTCAGAGGAGCCACCACGACGACGAGCGTCTCCCAAG	215113
Qy	2255	-----	2255
Db	215114	ACACCCCTAGCCCGGAGCGGTGAACCGCAGAGGAGATTTCAAGAGCCCGTGATCTTCTA	215173
Qy	2255	-----	2255
Db	215174	CCAGGCAGGGGATGCAGCGTGGGGCGGTGAAGTCTTCCAAATGTCTAAGGCATC	215233
Qy	2255	-----	2255
Db	215234	TCAGTGGTGAGTTCCCATCATCAAGGATGCAAGCTCGGCACCAAGTGAGTGATGT	215293
Qy	2256	-----ArgMetGlySerLysSerProGlyAsnThrSerGlnPro	2268
Db	215294	GAGGTGTTTGATCTCTACAGCAGGATGGGTCTCAAGTCTCCAGGCAACACACGACGCG	215353
Qy	2269	ProAlaPheSerLysLeuThrGluSerAsnSerAlaMetValLysSerLysLysGln	2288
Db	215354	CCAGCCTTCTTCAGCAAGCTGACCGAGAGCACTCCGCCATGGTCAAGTCCCAAGAGCAA	215413
Qy	2289	GluIleAsnLysLysLeuAsnThrHisAsnArgAsnGluProGluTyrAsn-	2305
Db	215414	GAGATCAACAAGAAAGTGAACACCCACACCGGAATAGCGCTGATACAG-TAAGGGGCC	215472
Qy	2305	-----	2305
Db	215473	TGCAGGCTCCCGGGAAGCATGGGCCACAGGTGGGGGTGGCCCTGCTGGGCGCTGG	215532
Qy	2305	-----	2305
Db	215533	AGCGGCCAGTGGCAGAAACCCAGGTGCACCTTCGAAAGCTAAGTGGCCCTGCTGACCA	215592
Qy	2305	-----	2305
Db	215593	CTCCCCCAGGCCCTTTGGCTCACATTTGGGGAGCCCCAGGGGAGTTTCTTGAATTGCT	215652
Qy	2305	-----	2305
Db	215653	GGCCTTTCCATAGAGCTTACTGCGCAGAGAAGATAGCACCAGCACATAGTAGTGCCC	215712
Qy	2305	-----	2305
Db	215713	AGTGAATACCTGCATGAATACTGGGACACGAGGGGTGGATCCCTCCACACAAGGGCGGG	215772

Qy	2305	-----	2305
Db	215773	CGCTCCACACTCAGCACCTGTGTGGCTTTGCACCCATTGACGTGTGTGGGTATGA	215832
Qy	2305	-----	2305
Db	215833	ACGCCCACTCTCTTTCCAGTCCCTTAGCAGCGCCTGGCAGTTAGCAGATCCACCAGG	215892
Qy	2305	-----	2305
Db	215893	GAATACGTGAGTGGTGGGCAATAAAGAAATCTGTACAGTCCCCGACCCCAAGAGCCT	215952
Qy	2305	-----	2305
Db	215953	CATCTGCCAGGAAGTTTGGACAAATCACAGATGCTTTTCCCTTCTCTGGGCTGGAGTAG	216012
Qy	2305	-----	2305
Db	216013	AAACCTTGCAGATAGTCACTGGCTTGC CGGCACGTGGTGCCTCATGCCCTATAGGCCACGA	216072
Qy	2305	-----	2305
Db	216073	CTTTGGGAGGATGAGGAGGAGGATTGCTTGAAGCCAGGAGTTTCGAGACCAGTCTGTGCA	216132
Qy	2305	-----	2305
Db	216133	ACATAGCAAGACCCCATCTCTACAAAAAACTTTAAAAACAGGCACACACCTATAGTCCA	216192
Qy	2305	-----	2305
Db	216193	AGCTCTGGGAGGCTGAGATAGGAGGATTCTTTGAGCCTCGGAGGTCAAGGCTGCAGTG	216252
Qy	2305	-----	2305
Db	216253	AGCTATGATCACACCTGCACCTCCAGCCTGGACAACAGAGCAAGACACTGTCTTAAAAA	216312
Qy	2305	-----	2305
Db	216313	AAAAAAATCTCTGACCCAGGCTGGTAACCTCCAGGGCCCTGTAAAGTGCAGTCCAGGAA	216372
Qy	2305	-----	2305
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Qy	2305	-----	2305
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Qy	2305	-----	2305
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Qy	2305	-----	2305
Db	216733	TGGCCCTGTCCCAGGCGCTGCTGCATGAGAAGCTGCAATGCACAAAGTTTCCCAGGTGATG	216792
Qy	2305	-----	2305
Db	216793	CCAGCACACCTGCGCTGGACCAACACGCGGACTGGTAGGGCAGGTAATTTCCAGAGACCTGG	216852

QY	2306	-----IleSerGlnProGlyThrGluIlePhe 2314	Db	217933	GAAGTAGGTCTAGACACACAGGTGTATCTGTGTGTAAGAACTCATGGCATGTCAGTGC 217992
Db	216853	GGCCCTCACCCACTCTGTACCGGCTTCAGATATACGCCAGCCTGGGACGAGATCTTC 216912	QY	2322	----- 2322
QY	2315	AsnMetProAlaIleThrGlyThr----- 2322	Db	217993	AAGATTATGCTAACTTATATATAATAATTTTGTATTTATCTTTTAAAGACACGGTCT 218052
Db	216913	AATATGCCCGCATCACCGGAACAGGTAACCATCCAGCCCTTGCTATATAGCTGCCCTG 216972	QY	2322	----- 2322
QY	2322	----- 2322	Db	218053	TTCTGTCACTAGGCCAGAGTGCAGTGGTGCANTCACAGCTCACTGCAGCTCCGGCTCC 218112
Db	216973	GTCCCTCCGCTCCCTCCCAACCCCTGCTCAGCTGTATGAAGGACGAGGAGCTTCG 217032	QY	2322	----- 2322
QY	2322	----- 2322	Db	218113	CAGCTTAGATGATCCTCTACCTCTCAGCCTCTCTGAGCAGCTGGGACTACAGGCATGCG 218172
Db	217033	CTAGTCTGGGTGTACCCCTCACTCTGGGTGAAGTAAACCGACAGTAGGATTCAGAGTC 217092	QY	2322	----- 2322
QY	2322	----- 2322	Db	218173	CCACTGCACCCGAGTAATTTTATCTTTTGTAGACAGAGCTCTCAATATGTTACCC 218232
Db	217093	ACACACAGCGAGCGAGGCTTGTTCCTGTGTAGACAGATCCTCGCTGTGCGAGGAAT 217152	QY	2322	----- 2322
QY	2322	----- 2322	Db	218233	AGGCTAGTCTTGAACCTCTGTCTCAAGCTGAGGATCTCCACCTCGACTGATTTTGT 218292
Db	217153	CTCTGGAGTTAAGATCCCTCGGGTGTAGTAAGTATCAGATGACCCCTCACAGCTGG 217212	QY	2322	----- 2322
QY	2322	----- 2322	Db	218293	TTTTGTCTTGTGTTTGTCTGTGTTTGTACAGAGTCTTGTCTCTGTCTGCCCCAGGCTG 218352
Db	217213	AAACTCACCTTGTCTTCGCGACCTCAGCTGGAGATGCACATGTCTGGACGAGGGTG 217272	QY	2322	----- 2322
QY	2322	----- 2322	Db	218353	GAGTCAGTGGTGCNACTTGTGGCTCACTGCAGCCTCTGCCTCCCGGTTTCAGCAGTTCT 218412
Db	217273	GGCTGAGCTCAGAGCACAAAGCCTCCGAGTTCACTCGGGGTTTGTATAGCTAGAGCTT 217332	QY	2322	----- 2322
QY	2322	----- 2322	Db	218413	TCCACCTCAGCCTCCCAAGTAGCGGATACAGACACCCGCCACTACACCTGGCTAATTT 218472
Db	217333	CATTCTTAATCCAGCCAGGGAAGCTTGGAGCCCTTACTTTTCTTCAAGATCAAATAC 217392	QY	2322	----- 2322
QY	2322	----- 2322	Db	218473	TTGTATTTTGTAGACAGCGGGTTTCATCATATTTGGCCAGGCTGATCTCGAACTCTGA 218532
Db	217393	AGGTGTGTGCAGAGATAGGTGTAATGTGACGCACTTTTAAGCTGAACCTTAAGACT 217452	QY	2322	----- 2322
QY	2322	----- 2322	Db	218533	CGTCAGATGATCCACCCACATTTGGGCTCCCAAGTGTGGGATTTACAGGCTGAGCAGT 218592
Db	217453	TCTATGATCTTTGGACTTAGGGGTCCCTTGAGGTTGGAGCCCATCCTCTAGGAGGGCC 217512	QY	2322	----- 2322
QY	2322	----- 2322	Db	218593	CACGCCACGCTGATTTTCTTTTATGCAGTTTATGTCAGTTTGTAGTCCACAAGAGAAATTTTCCAG 218652
Db	217513	CCATTGTGATTTTCTTGTGTGAGTCTGGGGTGTGGCCTCTGGGGGTCACTCTGCATGGGC 217572	QY	2322	----- 2322
QY	2322	----- 2322	Db	218653	GCTCCAGTCTTTGCCACTCAACCTGTGTGAGACTTCACTTTTATAATGGAGATCGTTAA 218712
Db	217573	AGCCCTGGCCAGTGGGGCTGAGGCAGTTTGGGGTCCGCTCTGTGTGGGTGCCTG 217632	QY	2322	----- 2322
QY	2322	----- 2322	Db	218713	GCCTGGAGCAGCTCCATCAGGTACGGACTCTGTGGCCTTGGGTAGAGGCCAGTCGCG 218772
Db	217633	GTTATCTCTGTGCTTGTGTGAAGCTGAGGCCAGGATGAGGTTCGGAGAGTTTGTCTG 217692	QY	2322	----- 2322
QY	2322	----- 2322	Db	218773	CTGCTGTGATTTCAGCACTCACCTTGTGGAAATGTTGCTTTTCTTCATGCACATGGC 218832
Db	217693	ATCTTCCCTGGGAACATCTCTGGGCTTGAGCCCTGGGAATGTTGAGGAAGATAGTC 217752	QY	2322	----- 2322
QY	2322	----- 2322	Db	218833	TGTTTTTCAAAAGTGTGCGAGAAATGTGGCCAAAGACAGCAGAGAAAGGTGTGAGCATCCC 218892
Db	217753	GTTCAGATATTACAGGGGTACAGGCGCTCCAAATGGGAGTCCCAACTAGACACCT 217812	QY	2322	----- 2322
QY	2322	----- 2322	Db	218893	TGGCTACAAAGTATTTGAAACCAAAAGGAAAGAAAGCCAGCAGCCAGCAGTTGCT 218952
Db	217813	CCACCTGCCAGTGAAGTACACCGGGGCAATGGCAAGCCTCAGGCAACGGGAAGAGA 217872	QY	2322	----- 2322
QY	2322	----- 2322	Db	218953	ACAGAAAGCTGATTTTCAAAGCATCTGCATCACCCGCAACCTCATGGAAGCCTCGGTTTG 219012
Db	217873	CAATTGGTCGAACAACAGAGGGTTAGAAATGAATGTTCTCGGATGTTCTAAATCTT 217932	QY	2322	----- 2322
QY	2322	----- 2322			

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Db	220153	CTTATGACCTATAGAAGCCAGCGGTGCAGGAACATGCAGCACCAATGGGGCTGGAG	220212
Qy	2344	AlaIleLeuArgLysAlaLeuMetGlyLysTyrAspGlnTrpGluGluSerProLeu	2363
Db	220213	GCCATATTAGAAAGGCACTCATGGTTAAATATGACCAGTGGGAAGAGTCCCGCGCGCTC	220272
Qy	2364	SerAlaAsnAlaPheAsnProLeuAsnAlaSerAlaSerLeuProAlaAlaMetProfile	2383
Db	220273	AGCGCCAAATGCTTTTAACCCCTCTGAATGCCAGTGCAGCTGCCCGCTGCTATGCCATA	220332
Qy	2384	ThrAlaAlaAspGlyArgSerAspHisnhrLeuThrSerPro	2397
Db	220333	ACCGTGTGACGACGAGGTGACACACACTCACCTCGCCAGGTCTGAGGCCACCCCC	220392
Qy	2397	-----	2397
Db	220393	GCCCCGCCCGCTCTGTCCCCACCCCGGTGTGATTAACTCTCGCTCTCTCCGCGCTCCTC	220452
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Db	220453	TGCAACCCCTCTCGAGCTTTGGAGCTTGTGACTTTATTTTGTGTGCTGTTGACCTC	220512
Qy	2397	-----	2397
Db	220513	GTTCTGGAGTTTGCTAATCTGAAGCTGGGCTGCACACCCCCCAAGTGTCTGTACCTCTGC	220572
Qy	2397	-----	2397
Db	220573	CCCCAGCCCCGGCCCTCTGCCCACTAGGCCGGAAGCGTGC CGCCTCCCTCGGACACT	220632
Qy	2397	-----	2397
Db	220633	CACACTGTGTCCGCCCCCAAGTCTCCCGCTTCTCTCCCTGGGGGAGCCCGGCTTCTTG	220692
Qy	2397	-----	2397
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Db	221113	GCCCTGGGGTGGGTCGTGCAGGACAGCCAGGGGGCTATTGCAACACGACGACGACT	221172
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Db 221233 TCTGGTCAACCTGGCTTCCAGCTGGGCGGGCAGCAGGAGGAGGGTTTACCTTACT 221292
QY 2397 ----- 2397
Db 221293 GCTCTCCCTCCCTCTTTGGAGGGCCCATGGCAGGACCTCACCCCTGCCCTGTGGCCCCC 221352
QY 2397 ----- 2397
Db 221353 CGTAGCGTGGTCTGCTCTTCACTGCCAACGACGCCCTTCCCATCTTGTCCCTCGCA 221412
QY 2398 GYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 2417
Db 221413 GGTGGCGGGGGAAGCCCAAGGTCTCTGGCAGACCCAGCAGCGCAAAAGCCCAAGTCCCGG 221472
QY 2418 AlaProGlyLeuAlaSerGlyAspArgProProSerValSerValHisSerGluGly 2437
Db 221473 GCGCCGGGCTGGCATCTGGGGACCGGCCACCCCTCTCTCTCACTGACCTCGAGGGA 221532
QY 2438 AspCysAsnArgArgThrProLeuThrAsnArgValTrpLeuAspArgPro----- 2454
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QY 2454 ----- 2454
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QY 2456 Ser-AlaGlySerThrProPheProTyraSerProLeuIleMetArgLeuGlnAlaGlyVa 2475
Db 222193 TCCCGCAGGTTCACGCCATCCCTTACAAACCCCTGTATCATGCGCGCTGCGAGCGGTGT 222252
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Db 222373 CAGCGAG 222379
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US-10-414-692-15
; Sequence 15, Application US/10414692
; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-Cepto Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; FILE OF INVENTION: Profile
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,650
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-414-692-15
Alignment Scores:
Pred. No.: 1.29e-123 Length: 2745
Score: 2184.00 Matches: 490
Percent Similarity: 62.89% Conservative: 110
Best Local Similarity: 51.36% Mismatches: 208
Query Match: 16.53% Indels: 146
DB: 15 Gaps: 26
US-09-522-753-5 (1-2517) x US-10-414-692-15 (1-2745)
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QY 156 ThrAppProGluLeuGluLeuValProProArgLeuSerLysGluGluLeuGlnAsn 175
Db 166 TGTGGAGATGATCAAAATGCTTCACCTTCAAAATCTCTAAGAGAGAGTTAATACAGAGT 225
QY 176 MetAspArgValAspArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLys 195
Db 226 ATGGATCGTGTAGATCGAGAAATTCGAAAAGTAGAACAGCAGCATCTTAAACTGAAAAAG 285
QY 196 LysGlnGlnLeuGluGluAlaAlaLysProProGluProGluProLysProValSer 215
Db 286 AAACAACAACAGCTTGAAGAAGGAGGAGCTAAACCTCTGAGCCTGAGAGGCCCTGTCTC 345
QY 216 ProProProIleGluSerLysHisArgSerLeuValGlnIleIleTyraSpGluAsnArg 235
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QY 236 LysLysAlaGluAlaAlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuPro 255
Db 406 AAAAAAGCAGAAGAGCTCATAAAATTTTGAAGGTCTTGGCCCAAAAGTTGAACATCGCA 465
QY 256 LeuTyraSerGlnProSerAspThrArgGlnTyraHisGluAsnIleLysIleAsnGlnAla 275
Db 466 CTGTATTAACAGGCATCAGATACCAAGTGTACCATGAGAACATCAAGACAAACAGGTG 525
QY 276 MetArgLysLysLeuIleLeuTyraPheLysArgArgAsnHisAlaArgLysGlnTrpLys 295
Db 526 ATGAGGAAAACCACTCAITTTATTTTAAAGAAAGAAATCATGCAAGAAACAAAGGAA 585
QY 296 GlnLysPheCysGlnArgTyraSerGlnLeuMetGluAlaLeuGluLysLysValGluArg 315
Db 586 CAAAAATCTGCCAGCGTTTATGATCAGCTCATGAGGCATGGGAGAAAGTGGACAGA 645

Mon Apr 19 08:15:06 2004

us-09-522-753-5.rnpb

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Db      2596  CTCTACCGGACACATTAAGCATGTCAGTCTCCTCGAG----- 2643
QY      993  LysProAlaProProAlaProProProGlnAsnLeuGlnProGluSerAspAlaPro 1012
Db      2644  -----GAGCAGCGCGCAGAGACAAGACATAGATTGGAA 2679
QY      1013  GlnGlnProGlySerSerProArgGlyLysSerArgSerPro 1026
Db      2680  TGTAGAAGTTCTACAAGTCCATGTCGCACATCCAGAGTCCA 2721

RESULT 16
US-10-174-014-12
; Sequence 12, Application US/10174014
; Publication NO. US20040005292A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
; FILE REFERENCE: PFS-0012
; CURRENT APPLICATION NUMBER: US/10/174,014
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 12
; LENGTH: 221000
; TYPE: DNA
; ORGANISM: H. sapiens
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QY	1036	AlaAlaGluAlaGlnLysLeuProGlyAspProCys-----	1048
Db	191539	GGCCACACGAGCAATGGTTGAAGAAGCCGAGAGCCTGTTCAGTTGCTCATTCCTCTGAG	191598
QY	1049	---TriThr-SerGlyLeuPro-----PheProValProPro	1059
Db	191599	GGGTGGG-CGGGGCTCGCGGGCTCAFTTCTGATAGCTCTGGACTCGGTCGCCCTGGGA	191657
QY	1060	ArgGluValIleLys-----AlaSerPro-----HisAlaProAspProSer	1073
Db	191658	AGAGAGCCCTGGCTAGATGGGGAAGACCCACGCTTACCTTCGGGGGCCACCTCCGTCT	191717
QY	1074	AlaPheSerfyrAlaProProGly-----HisProLeuPro-LeuGlyLeuHisAspTh	1091
Db	191718	GTTACCTCTCTGCCTCGGGGACAGTGAGCGGGGCCCATGTAGGCTCTCTTGGCCT	191777
QY	1091	rAlaArgProValLeuProArgProProThrIleSerAnProProProLeuIleSerSe	1111
Db	191778	GGCGAGCCACCCCTGCCACCCCTCCACCTCCACCTGCCTGCAC-	191817
QY	1111	rAlaLysHisProSerValLeuGluArgGlnIleGlyAlaIleSerGinglyMetSerVa	1131
Db	191818	-ACACACTCTCCGTGCACAGCAGACTTGTGTGGGCACTCATCATGCACATCGC	191873
QY	1131	Ighn-----	1132
Db	191874	ACAGTTTCTGGGTGCACACGTGTATACATAAAGCCGTGTACTGCTGCACCCCTGGT	191933
QY	1133	-----LeuHisValProTy	1137
Db	191934	ACATGTGTATACAGCACCCACTTAGTPTFCAGAGCCAGGTCACGTGCATGTGCCAC	191993
QY	1137	rSerGluHisAlaLysAlaProValGlyProValThrMetGlyLeuPro-----	1153
Db	191994	ATCCACTCTGCACACACAGACCCGTGCCAGTGCACATGCGTCTCCTGCCTGCCACAC	192053
QY	1154	-----LeuProMetAspPro--	1158
Db	192054	GTCCACACACTGCTGATGTATCGGTGCACACGGGTGCTCTGCTCGCCGCCACCTCCACT	192113
QY	1159	-----LysLysLeuAlaPro-----	1163
Db	192114	CTGCTGTATCGGTGCACGCGTCTGCTGCTGCCACATCCACATCTGCTGCTGATGT	192173
QY	1164	-----PheSerGlyValLysGlnGluLeuSerProArgGl	1176
Db	192174	ATCGGTGCAGTGTCTCTCCCTGCCACACATCCACACACTGCTGATGCGTCTTGCTC	192233
QY	1176	yGlnAla-----GlyProProGluSer-----LeuGlyValProThrAl	1189
Db	192234	ACGTGCATGTGTGCATTTGTTACGCCCCATGTCCGCCACCCGCGGTGTGGACACAGA	192293
QY	1189	aGlnGluAlaSerValLeuArgGlyThrAlaLeu-----GlySerValProGlyGlySe	1207
Db	192294	CTCAGCTGCTATGTGGTCAAGGACACCCCTCTCTGCAGACAGACACCTCTGGAGGCG	192353
QY	1207	rileThrLysGlyIleProSerThrArgValProSerAspSerAlaIleThrTyrArgGl	1227
Db	192354	TAGGGTACAGGTGCAGGACGGTCCCTGCATCTCCACCGTGCACACCCCTCGAAAAG	192413
QY	1227	ySerIleThrHisGlyThrProAlaAspValLeuTyrLysGlyThrIleThrArgIleIl	1247
Db	192414	CTCCTGG-----GTCTGCTGCAGGGCCCC-----CA	192440
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QY	1263	-----LeuProLysGlyHisValIle-----Ty	1270

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Qy	1356	-----	1356
Db	193761	ACTCCTGAGCTCAAGCTGTGCTGCGCGCAGCCCCCAGAGATGTGGATTACAGCGGT	193820
Qy	1356	-----	1356
Db	193821	GAGTACTGCACCAGCCTGTGGTTTTAGCTTCATGATTTTCATAGTGTTCCTCCGACTTGT	193880
Qy	1356	-----	1356
Db	193881	GAGTGGTTTCAATATTTCTGTTTATGTGTGAAGAAGCTGAGGCCCCAGAGAGTCA	193940
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Db	194001	AACCCACTGGTGTGGAGCTCTTGATGGTCTGGTGGGGCGGCGTGAGGTCAGTGC	194060
Qy	1357	-----GlnGlyIleProArgSerTyrValGluAlaGlnGluAspTyrLeuArgA	1373
Db	194061	TGTCGGCCCGGCGAGGATC-CCTCGTCTACGTGGAGGCACAGAGGACTTACCTGGCTC	194119
Qy	1373	rgGluAlaIysLeuLeuIysArgGluGlyThrProProProProProSerArgAspL	1393
Db	194120	GGGAGGCCAAGCTCTTAAGCGGAGGCGCGCTCCGCCGCCACCGCTTCAGGGACC	194179
Qy	1393	euThrGluAlaTyrLysThrGlnAlaLeuGlyProLeuLysLeuLysProAlaHisGluG	1413
Db	194180	TGACCGAGGCTCAACAGCGCAGGCCCTGGGCCCTCTGAGCTGAGCGCGCCATGAGG	194239
Qy	1413	lyLeuValAlaThrValIysGluAlaGlyArgSerIleHisGluIleProArgGluGluL	1433
Db	194240	GCCTGGTGGCCACCGTGAAGGAGCGGCGCTCCATCCATGAGTCCCGCGCAGGAGC	194299
Qy	1433	euArgHisThrProGluLeuProLeuAlaProArgProLeuLysGluGlySerIleThr-	1452
Db	194300	TGCGGCACACGCCGAGCTGCCCTTGGCCCGCGCGCTCAAGGAGGGCTCCATCAGC	194359
Qy	1452	-----	1452
Db	194360	AGGTATGGCCCGGCGGACACACGGGCCAGTTCTTAGGAGGGTGGCGGTGCTGTGG	194419
Qy	1452	-----	1452
Db	194420	GGCACTGCCCTGGGCTCTCCACATGGGGAACCGAGGCTGAGAGCCTCGGTACCTTA	194479
Qy	1452	-----	1452
Db	194480	CAGTACCCAGCTGCTCATCACCGGGCTCAGCTGTGCTGTTCACGGGCTGGCGAGGG	194539
Qy	1452	-----	1452
Db	194540	GCACCGGCTCTGACCTGATTCTACTGAACCTACATGTTTCCCATTTCTTCAGGGAGGA	194599
Qy	1452	-----	1452
Db	194600	AACTAGTCCCAGAGAGGCCAGGCAGCTTCCAGGCCACAGGACTAAACATAGTGACGA	194659
Qy	1452	-----	1452
Db	194660	GTAATGCTCCCTCGTTGAATCTTTGTGAGGGTCCAGGTGCGGCTGAGGATGTTGTCATGC	194719
Qy	1452	-----	1452
Db	194720	TTCAATGTTTCAACCCCTAGCAATGCTCTGAGTGTGTTTCTTAATGACCTTAATTTATT	194779
Qy	1452	-----	1452
Db	194780	GCTGAGTAAATTTGAGGTTTCAGAGAGGTTCAACGACTCACCCAGAGTCACGAGCAAAATGC	194839
Qy	1452	-----	1452
Db	194840	AGTTGTGAACCCAAATTCAGATGTTCTCAGCGCGCAGCATCCACTGCACCCACACGCA	194899
Qy	1452	-----	1452
Db	194900	GGTTGCACCAAGAGGCCCGAGTCCCCCAGCGCGGCCAGCTCAGTAGGGGAAGTTCC	194959
Qy	1452	-----	1452
Db	194960	GTGCCGATGGTACGAGGACGAGGAGTGTTCGGTGGAAAGCCCCCTGAAGGCCACTGTCT	195019
Qy	1452	-----	1452
Db	195020	TCCACATGGGCGAGGTGGCTCTTTGTGAAGGGGAAGAGATGGGAGCCACACGGGGC	195079
Qy	1452	-----	1452
Db	195080	TGTGGGCTGTGAGCGGAAGGACTGGGGTGGGTGTCCCGGAGGGGTTCCAGCTTGTAG	195139
Qy	1452	-----	1452
Db	195140	GAAGTGTGTAAGCCAGGAGGAGGAGCAGAGATCCTGATTTGTCAGGGGAAGG	195199
Qy	1452	-----	1452
Db	195200	GTTTGGCTCTCAGCCCCCTAGGCAATATATGAGTCTTGGAAAGCATCCACCGCATGACCA	195259
Qy	1452	-----	1452
Db	195260	GACAGGTCCAGATTCTAGAATATTTCTTTGAAAAACAAGGCGAGTTCCCTCTTACGA	195319
Qy	1452	-----	1452
Db	195320	CAGTAATGAAGACATCCCTAAATAGAGTTTTTGTGTTGCAAAAGCCCTAAAGTCCCA	195379
Qy	1452	-----	1452
Db	195380	TATCAAGTGTCTCGAAGCCTGTGAAAAGAGGAGGGGACCTGTGGCTGGCTACGAA	195439
Qy	1452	-----	1452
Db	195440	GGTCCAGTCTGGACTGTGACCCCCCATTTCTCACCATCTTCTGTCTGGAGGGCAA	195499
Qy	1452	-----	1452
Db	195500	ACACCTCAGCCCTGACCTCAGTGTCTCCCTGGGGCTGAAAAGCCTCAGGGCGGTAGTATGG	195559
Qy	1452	-----	1452
Db	195560	GTCTGGGTGTGACTTTTCTGCTTGGCATTTGGGTGGCCCATGAGGGTCCAGGCTGAA	195619
Qy	1452	-----	1452
Db	195620	CAGAGGAATGTTTTTACCCACATGAGGGTGTGGGCTTCTTCTCGCAACTCCAGGA	195679
Qy	1452	-----	1452
Db	195680	CCATCAGAGAGCCCACTCGCGGCAGGAGAGTTGACTGTGAACTTTTACCCCTTT	195739
Qy	1452	-----	1452
Db	195740	CTGAGTCCCCCAGGAGCGTGGGGACACAGGCTCAGGGTCCAGGCCAGGCGATGAA	195799

QY	1452	-----	1452
Db	195800	GTAAACAGTGTGCCATCTCAGGGTTAGCAAAGCCCTCTGTCTCCCTGCTCTGGAGGCAT	195859
QY	1452	-----	1452
Db	195860	CAGATGTCACTTCCATCTTATAGATGACAAACTTTTGTAGGCTCAGAAGGGGATGCAGC	195919
QY	1453	-----GlnGlyThr	1455
Db	195920	TGTTCTGGGCTATGGCTGTGGCCAGGGCTAGAGCTTACATCCCTCTGCCCCAGGGCACCC	195979
QY	1456	ProLeuLysTyrAspThrGlyAlaSerThrGlySerLysLysHisAspValArgSer	1475
Db	195980	CCGCTCAAGTACGACACCGCGCGCTCCACACTGGCTCCAAAAGACGACGATCCCTCC	196039
QY	1476	LeuIleGlySerProGlyArgThrPheProProValHisProLeuAspValMetalAsp	1495
Db	196040	CTCATCGGCACCCCGCGCGACGTTTCCACCCGTGCACCCGTGGATGTGATGGCCGAC	196099
QY	1496	AlaArgAlaLeuGluArgAlaCysTyrGluIuSerLeuLysSerArgProGlyThrAla	1515
Db	196100	GCCCGGGCACTGGAACGTCCTGTACAGAGAGACCTGAAGACCGCGCCAGGGACCGCC	196159
QY	1516	SerSerSerGlyGlySerIleAlaArgGlyAlaProValIleValProGluLeuGlyLys	1535
Db	196160	ASGAGCTCGGGGGGCTCCATTGCGCGCGCGCCCGCTCATTTGTGCTAGCTGGGTAAAG	196219
QY	1536	ProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaGlyHisLeuPro	1555
Db	196220	CGCGGGCAGAGCCCTTACCTATGAGAGACACGCGGCGACCCCTTTGCGCGCACCTCCCA	196279
QY	1556	ArgGlySerProValThrMetArgGluProThrProArgLeuGlnGlySer	1573
Db	196280	CGAGGTTTCGCGGTGACCACGCGGAGCCACCGCGCGCTTGCAGGAGGTGA-GTGGGG	196338
QY	1573	-----	1573
Db	196339	TGTGCATGGCGGTGAGTGGGTGGCGCTGTCTGGAGAAGCTGTCTCCCATCCACCC	196398
QY	1573	-----	1573
Db	196399	ATTAGCTTAGTTTGCACCTGGGATATCTCGCCACCCCGCTTCCACCATCCAAACCAC	196458
QY	1573	-----	1573
Db	196459	CTGCAGCCGCTGGGCTCGCTCCGATTCCAAACCCCTGTCCAACTCTTGCCACCTCCC	196518
QY	1573	-----	1573
Db	196519	AGACCACCGTGTGTCTCACTAGTTCCTCCCAAGCCCCCTCCTCTTCTGCTGTATCC	196578
QY	1573	-----	1573
Db	196579	ACTCTGAAACAGCTACCCGGATCTTTCTTAAATATGCAATATATTTCCACTTCCC	196638
QY	1573	-----	1573
Db	196639	TGCTTCCATCCTTCTAGCAACTTACACATTTTGTCTATGGCCTTGGGGCGCCTGCTGTT	196698
QY	1573	-----	1573
Db	196699	GGGGCCCTGCCTCTCATTCAGCGGGATTCCTTCCTCCCGACCCCGACGCCCTG	196758
QY	1573	-----	1573
Db	196759	GGCCCTCTTCTCTTTGTTCCCTGGCCATCTTAGCTCGGTCAATTCAGTATTTGCTGGG	196818
QY	1573	-----	1573
Db	196819	GGCCTTTGCGTGGGCTCTCTCTCTGCTGCCATGTCCCGCCTTCCAGATCTTTACTTA	196878
QY	1573	-----	1573

D	b	196879	GTGGTTTCTTCCATCCCTCAGGTCTTTGTGTTTACATATTACATCTCTGGGAGGCTTCT	196938
Q	y	1573	-----	1573
D	b	196939	AACCAGACCCCTATCTCCAGTTTCATATCACATGCTGTGACATTTTAAATTTCTCTCCG	196998
Q	y	1573	-----	1573
D	b	196999	GCCAGGCATGGTGGCTCACACCTGTAATCCACGACGTTTGGGAGGTCAAGCGAGGAGAT	197058
Q	y	1573	-----	1573
D	b	197059	CACCTGAGGTGAGGAGTTCAAGACCGCTGGTCAACATGGTGAAACCCCTGTCTCTACTTA	197118
Q	y	1573	-----	1573
D	b	197119	AAAATACAAAAAATAACCGGTGTGGTGTACGCACCTGTATTCACGCTACTCTGGGAG	197178
Q	y	1573	-----	1573
D	b	197179	GCTGAGGCAGGAGAATCACTTGAGCCTGGGAGGCAGAGGTTACAGTGAACGGAGATCGTG	197238
Q	y	1573	-----	1573
D	b	197239	CCATTGCATCCAGCTGGGCAACAGAGTGAAACTCTTATCTCAAAAAAATAAATAAAT	197298
Q	y	1573	-----	1573
D	b	197299	GAAGAAAAATTTCTTCTGAGCGTGTTCACCTCTGTAATTCATTTGTTGTTGCTAGTTTA	197358
Q	y	1573	-----	1573
D	b	197359	TCACCTGTCTCGCAATTGAATGTACGTTGTGAGGCTGGGATTTCTGTTCCTTCACT	197418
Q	y	1573	-----	1573
D	b	197419	GGGTGACCCCGATTCTCAACAATGCTTGCCAGTAGAGGCTGCATCAATATTTT	197478
Q	y	1573	-----	1573
D	b	197479	TTAATTGATTGAGTGAGTGAATGAAGATGAATGAATTTTAAAAAACTATACACAAA	197538
Q	y	1573	-----	1573
D	b	197539	AGCAATGAGTCAGTGAGCAAAAAGTAACTAAGGCAATGAAGAAATGAAGAGTGAATG	197598
Q	y	1573	-----	1573
D	b	197599	AAGAGACCTGGTCTTGGGATCCGAGGTCCCTATCTCTCAACAACTCCCCGTAATGCC	197658
Q	y	1574	-----LeuSerSerSerIlys	1578
D	b	197659	AGCCCCAGAGGCCCGATGCATCCACCTTGCCCGTCCACAGGCGCCTTTGCTCCAGCAAG	197718
Q	y	1579	AlaSerGlnAspArgIylsLeuThrSerThrProArgGluIleAlaIylsSerProHisSer	1598
D	b	197719	GCATCCAGACCGCAAGCTGAGTCGCGCCTCGTGAATGCCAGTCCCGCACAGC	197778
Q	y	1599	ThrValProGluHisProHisProIleSerProTyrGluHisLeuLeuArgGlyVal	1618
D	b	197779	ACCGTGCCGAGCACCCACACCCCACTCGCCCTATGAGCACCTGTCTGGGGCGTG	197838
Q	y	1619	SerGlyValAspLeuTyrArgSerHisIleProLeuAlaPheAspProThrSerIlePro	1638
D	b	197839	AGTGGCTGGACCTGTATCGACGCCACATCCCCCTGGCCTTCGACCCCACTCCATACC	197898
Q	y	1639	ArgGlyIleProLeuAsp	1644
D	b	197899	CGCGCATCCCTCTGGAGCGCAGGTGATTGCCCTGGGCTCCACAGAACCTGCAGTGTGC	197958
Q	y	1644	-----	1644

[illegible]

Db	202336	CTTGGCTATTAAACATTGAGCAATGTTACATATGCAAAATTTCTGTAGATGGCTTGAATTAC	202395
Qy	1898	-----	1898
Db	202396	TCCCATAAATGGGGTATTCTTTTCTAGTCATGGACAGACTGCAATATTCTTAAACTTTT	202455
Qy	1898	-----	1898
Db	202456	TATGCCCTGCTTCCCTTTAAATATACTCTCAGTTTCAGACATCTCATTGCTCACACAT	202515
Qy	1898	-----	1898
Db	202516	ATGACCATATGCTGTTAGAACATCCAGGCGACATCTTCAATGCTTTGCTGCTCAGTGTG	202575
Qy	1898	-----	1898
Db	202576	TGGGGTGTACTACAATACATTTCATGCTTATATACAATGCATTTGAGGTTGAGGCATGTA	202635
Qy	1898	-----	1898
Db	202636	AAATACTAAGGCACGTGTGTATGTTGTTGTGCATGATACTGTAACCTCTGTCTCTG	202695
Qy	1898	-----	1898
Db	202696	AAACAGTACAGGAACAGGATGTGTGATAGGAGTGTGAAGACAGCATCTTAAGAAATG	202755
Qy	1898	-----	1898
Db	202756	TGGTTGATGCTTCAGATGAATAAATAAGTCCATATGACCTCATGCTGCCCCCAATAGC	202815
Qy	1898	-----	1898
Db	202816	CACCTGTGTGAATTTATACTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	202875
Qy	1898	-----	1898
Db	202876	NN	202935
Qy	1898	-----	1898
Db	202936	NNNGTTAGTCTCCTTCAGSATCTTTGTACGCGAGCCTGTGGTCTCTTATCATTTG	202995
Qy	1898	-----	1898
Db	202996	CTTGTCTGTAAAGGATTTTATTCTCTCTTCTTATGAAGTTTAGTTAGCTGATGTA	203055
Qy	1898	-----	1898
Db	203056	AATTCAGTAGAAAAATTTTCTTTAAGAAATCTTAAATATTGCCCCCCACTGTCTTCT	203115
Qy	1898	-----	1898
Db	203116	GACTCATAGGTTTCTGCAGAGAGATCGGTGTTAGTCTGATGAGCTTCCCTTGTGGTA	203175
Qy	1898	-----	1898
Db	203176	ACCTGACCTTCTCTGCGTCTTAAACCTTTTCTTATTCAACTTTGGTGAAT	203235
Qy	1898	-----	1898
Db	203236	CTGATGATTATGCTCTTGGGTTACCTTCTCTAGGAGTGTCTTTGTGGTCTCTGTA	203295
Qy	1898	-----	1898
Db	203296	TTTCCCGAATTTGAATTTTGGCTGTCTGTAGTTGGGAAGTTCTCTGGGATAATAT	203355
Qy	1898	-----	1898
Db	203356	CCTGAAGAGTGTTTTCCAACTTGCTTCCATTCTCCCATCATCTTTTCAGGTACCAAGC	203415
Qy	1898	-----	1898
Db	203416	AAATGTAGATTGGTCTTTTTCATAGTCCCATATTTCTTGGAGGCTTTGTCTTCTCTT	203475
Qy	1898	-----	1898
Db	203476	TTCAATCTTTTCTCTAACTTGTGTTTTCACATTTTATTTCAATTAATTGATCTTCAGTC	203535
Qy	1898	-----	1898
Db	203536	GCTGATATCCTTTCTTCCACTTGATTGATTGGCTATTGACACATGTGTATATCTTACGA	203595
Qy	1898	-----	1898
Db	203596	AGTTCTCATGCTGTGTTTTCAGCTCTATCAAGTCATTTATTTCTACTCCTCAAACTGTTT	203655
Qy	1898	-----	1898
Db	203656	ATTCTAGTTAGCAATTTATTTAATCTTTTCAAGGTTCTTAGCTTCTTGCATTGGGTTT	203715
Qy	1898	-----	1898
Db	203716	AGAACATGCTCTTTTAGCTCAGAGGAGTTGTTATTACCCACCTTCTGAAGCCTACTTCT	203775
Qy	1898	-----	1898
Db	203776	GTCAAITTCATCAAACTCATTTCTCCATCCAGTTTGTTCCTTGTGGGAGGAGTTGTGA	203835
Qy	1898	-----	1898
Db	203836	TCCTATGAAGGAGAGAGACATTTCTGGTGTGGGAAATTTTCAGTCCTTTTGCACCTGTTT	203895
Qy	1898	-----	1898
Db	203896	CTCCCATCTTCATGGATTATCTACCTTTGGTCTTTGATGTTGGTGACCTTTGGATGGG	203955
Qy	1898	-----	1898
Db	203956	GTCTCTGAGTGGACATCTTCTGTGTGATGTGATTTATCTCTTCTTGTGTTAGTTT	204015
Qy	1898	-----	1898
Db	204016	CTTCTTAACAGTCTGGCCCTCTCTGCTGAGGTTTGTGCTGAGTTTGTGGAGTCCACTCC	204075
Qy	1898	-----	1898
Db	204076	AGACTCTGTTTGTCTGGGTATCACTAGCGAGGCTGCAGAACAAAGATTGCTGCTG	204135
Qy	1898	-----	1898
Db	204136	TTCTCTCTCTGCAAGCTTCTTCCAGAGGACACCCACAGCTGCCAGCGGAGCTCTT	204195
Qy	1898	-----	1898
Db	204196	TTGTATGAGGTGTCTGTTGGCCCCCTGCGAGGTGTCTCCAGTCAGGCAATGTGGGT	204255
Qy	1898	-----	1898
Db	204256	CAGGACCCGCTTGGAGGAGCAGTCTGTGATGAATATTCTCANNNNNNNNNNNNNNNNN	204315
Qy	1898	-----	1898
Db	204316	NN	204375
Qy	1898	-----	1898
Db	204376	NN	204435
Qy	1898	-----	1898
Db	204436	TGCACCAATATGACCAACAAATTTCTTGTATATTTTTTAAGAGATGGATCTTACTACG	204495
Qy	1898	-----	1898
Db	204496	TGGTACAGGCTCAGCCTCCCAAGTAGCTGGGATTATAGTAGAGCCACACACCAGC	204555

QY	1898	-----	1898
Db	204556	CCAAATTAGATTGTTCTTAAGAGATATTCTGACCAGCCTTTAAATATCTAATCATAG	204615
QY	1898	-----	1898
Db	204616	TCACCTACTGAAAAACCGTCCCTTGACTTCGTGATTAGTTTCCTATTGCTGCTGAACACA	204675
QY	1898	-----	1898
Db	204676	AACCTTAGTGGCTTAAATGGCACAAATGATTGCTGACAAATCTGGAGGTGAGAACTTA	204735
QY	1898	-----	1898
Db	204736	GAATGTGCTCACTGGGCTAAACCAAGATGCCAGGCTGCGTTCTCTTCTGAATGCCTAG	204795
QY	1898	-----	1898
Db	204796	CGGGAATTCATTGCTTGCCCTTTTACCACCTTCCTTGGAGAAGGAGTCTACATGCTTTT	204855
QY	1898	-----	1898
Db	204856	TTGGCGCATGCCCTCTTCTGTAATCAAGCTAGCAATGCGTTGGATCTTTCTCAAA	204915
QY	1898	-----	1898
Db	204916	CTCTATCACTGACCTGCGCTCTGCTCTTCTACTTTTAACTGATGCTGTTGATCCATTGGGA	204975
QY	1898	-----	1898
Db	204976	TTGCTGGAATACTCAGGATAGTCTCTTATTTAATCACTCAACTGTTTAAACAACATTAAAC	205035
QY	1898	-----	1898
Db	205036	TCGCTCTTTAACTCTGGTTTCTCTTGTCTATGTGACATAAGACACTTACAGTTTTTCAGG	205095
QY	1898	-----	1898
Db	205096	GTTAGGATGTGGACATCGTGGAGGGAGACATTATCTCTACCACATGCTTCCAGTAT	205155
QY	1898	-----	1898
Db	205156	CTAGCAACCCATCTGTGCTGCTGGTCTTTCTACTGTGGGTGCGAATTTACTCTCCA	205215
QY	1898	-----	1898
Db	205216	GCCTTACCCCCAAGACCTCATGTGATGTGCGCTCGAGTTCACACACACAGTCCATC	205275
QY	1898	-----	1898
Db	205276	CAGATCCCCCAACACACCCCACTCACACAGCTCATAGCATTTGTTCTTGCAATTTTATC	205335
QY	1898	-----	1898
Db	205336	TTCTTTGATGTTCTCTTATCTCCAGCTGCTCCCTTTACTACCAACCAAGATGAATC	205395
QY	1898	-----	1898
Db	205396	TGTTTATCCTCGACTTATAGCAATGCATCTTCTCCATGAAGCTTTCCCTTAACCTTT	205455
QY	1898	-----	1898
Db	205456	TTCCCTCTGGATGTTTATATATATAATTTGTGACCTCTCTGTANNNNNNNNNNNNNN	205515
QY	1898	-----	1898
Db	205516	NN	205575
QY	1898	-----	1898
Db	205576	NNNNNNNNNNNNNNNNNNNNNTTGAATTTGTGGGTGTTGCTGGCGTTAAGTAGTAG	205635
QY	1898	-----	1898

Db	205636	GTAAGTGGGAGGAAAAAGAAATGCCCCAGATTAGCCAATGTGAAGAAAAAGATGGGGGG	205695
QY	1898	-----	1898
Db	205696	TGNTAAGTTAGGAAGGTAGGGGGGTGGGGAGAGATATAGACGCTGGCTTAGNTGGGGG	205755
QY	1898	-----	1898
Db	205756	GTGGATGGGTGGGTAGGGTTAGGGAGGTAGNTGGTGGGTGAGAGATATAGATGGCTG	205815
QY	1898	-----	1898
Db	205816	GGTTAGCTGGGTGGGTGGATGGGTGGGTGGGTAGGGTTAGGGTATGGAATGGA	205875
QY	1898	-----	1898
Db	205876	TGTTGGATGAGTAATTTGTGGGATGAGTGGATGGAGCCCCAGTGGATGGACGATGAT	205935
QY	1898	-----	1898
Db	205936	TGGCGGTGGGATGAGTAGATGGGAGGTGTTGTTGGTTTGAGAAATAGAATCTGTGGAG	205995
QY	1898	-----	1898
Db	205996	GGAGAGACTGAATGGGACTGTGAGAAAGACTTTCCCGGTCCCCACATTTAGCAAGC	206055
QY	1898	-----	1898
Db	206056	CAGCAAGGAAAAGAGGTGTCCTCTTGCTGCGACAAAGTCCCAAGTTTCTCTGAGATGG	206115
QY	1898	-----	1898
Db	206116	AGAGGCCCTGAGTGCCTCTGTGTACACACACTCCAGAGACTGTGGGAGAGCTGCTTC	206175
QY	1898	-----	1898
Db	206176	ACCAGGGGGTGGGTGTCACACCTCAACACCTTCCCTGCCCGGAACCTTTTTTTTTTT	206235
QY	1898	-----	1898
Db	206236	TTTTTTGATGAGTTGTAATCTGTCGCCAGGCTGGAGTGCAGTACGATCTCTGCTT	206295
QY	1898	-----	1898
Db	206296	ACTGCAACCTCCACCTCCTGGGTTCAGTGAATCTCCTGCTCAGCTCCCAAGTAGCTG	206355
QY	1898	-----	1898
Db	206356	CAGTTACAGCAGTCGCAACCAACCCGGCTAATTTTATATTTTATAGTAAATCGGT	206415
QY	1898	-----	1898
Db	206416	TTCAACACGTGGCCAGGCTGTCTCAAACTTCTGACCTCAAGTATGCTGCTGCTCAG	206475
QY	1898	-----	1898
Db	206476	CTCCCCAAGTGGCGGATTAAGCGGTGCGCCACCGCACTCAGCCTCCAGGACCTATTT	206535
QY	1898	-----	1898
Db	206536	AGAGGCAACTTACTCTCTCCAAATGAATTTTCATTCAAAAAAGTACTTGTGCCCCA	206595
QY	1898	-----	1898
Db	206596	GCCGCTTGGATGCTGAAGTACATCTCCCTTAATCATTTTCAATTATGAATAATGGC	206655
QY	1898	-----	1898
Db	206656	ATCGTTTCCCAAAAGCAGTGGCGACTTTGTCACCCCTGACTCAGACCCAGCGTGCATG	206715
QY	1898	-----	1898

Db	206716	AAGCACTAATCCCTGGCTGTGGGAGCAGAGGTTCCGCACACAGGCTCTGTGGGATATGCC	206775	Qy	1996	ArgThrProAlaLysAsnLeuAlaProHisLeuSerProAspProProAlaProPro	2015
Qy	1898	-----	1898	Db	207856	CGCACCCCTCGAAGAACCTCGCACCTCACACGCCAGCCGCGCGCCACCT	207915
Db	206776	CGTGACAGCCGATTCAAAATATATAATCGAGAAAACGAGTGCTGCCCACTGCCCGCTCAT	206835	Qy	2016	AlaSerAlaSerAspProHisArgGluLysThrGlnSerLysProPheSerIleGlnGlu	2035
Qy	1898	-----	1898	Db	207916	GCCTCGGCCTCGGACCCGCAACCGGAAAAGACTCAAAGTAAACCTTTTCCATCCAGGAA	207975
Db	206836	GAATGAGGCTCTGGGAGGTAGATTAGCGAGATGGGGTGCCCCATGGAACGCAGG	206895	Qy	2036	LeuGluLeuArgSer	2040
Qy	1898	-----	1898	Db	207976	CTGGAATCTCGTTCTCTGGGTAAAGACCACTGACAGCGGCCACCTTTCATAGACGCGATT	208035
Db	206896	GCTCCGGGAAGGCCACGTGGGTGAGCAGCGCGGCTCCTGTTCCAGCCCCAGCCCTGTGCA	206955	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208036	ATCATGGTCAAAATTGCTCACGATAAAGGGGCGGAGAGAGGTGGCTGGCCAAACGGC	208095
Db	206956	GGGCGAGCTGTGCCCAAGCTTCTCACTCACAGAGCTGGGAACAGAGCTTTCCTGTCT	207015	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208096	TCCCTCGCATGTGAAGACTTTCGGGCCGCGACCCACCCGCTCTCGTGTCCAAGATAT	208155
Db	207016	CAACGCCACCTGGCGGCCCTGGCATCCTTCCCTTGTCTCTCACTCCTCAAGTGG	207075	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208156	TTTCAGATCTCTGCTTTTACTTTTGGCCCCCGTTTTTTTGTGTTGGTTTGTGTTATTTT	208215
Db	207076	CTTTTGTAGCTCTTTCGGGTATCTCTGAGCAGGCCAGCTCCCTCATGTGCCCTCCCTGA	207135	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208216	GTTTTGAAGCCCATCCGTCCTCGCGGTTTGCACGCGTGACGACTACTCGGCGCGGCC	208275
Db	207136	AGACCTCCTAGCCCTGCTCAGCTTCCTTGCGGTTCTCTCTGTTACTCATTTGACTACC	207195	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208276	TGCCCTCTGTTTGGGGGCGCTCATCATTTTGACATCATTTTACCATTGTTTTTTTTTT	208335
Db	207196	TCCACACAGTTACCAGGCTCTGTAGAGCTTGGGATATCTGTTAATGTGATGCTGTCT	207255	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208336	TTGGAATTTTGTCTTTTCTTTTAAATGAATGAATCTGTGATCTGACTTGCAGCTCGGCC	208395
Db	207256	TTTCTGAATTAGATGGTAAGATGCTTGATCCGTTTTTATGACCGCTGTATTTCACAGTGC	207315	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208396	CCCATCTCCCTCTTTGGCGCTGTGTCCAGGAGCAGGATGGGGCTGGGGAGGCTCGG	208455
Db	207316	TAGAACAGTGCTGGCACCTAGTAGTCTTAATCAGAAAGTTTGGAAATGATGCAAGGAA	207375	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208456	GCCTACGCCCCACCTCGCGGCTGCTGTGATGCTGTGCACTGGGGGAAAGTGAGGAGG	208515
Db	207376	TGAATGAACGAATGATGGGATGGTCAAACCATGACGACAGAGTCTGGCAGGTTACAG	207435	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208516	CGGTGCAAGGAGAAGCTGAGGGGGGGGACGGGACCTGCGCTGTGAGGAGAGCTGGGTCT	208575
Db	207436	TCAGGAGGCGATTTTCACTCTGGGAGCAGCAGGGGATGTGGATTTATCCAGGGCAATGG	207495	Qy	2040	-----	2040
Qy	1898	-----	1898	Db	208576	GGCTCTTGCACTTTGCCCTGTCCCCAGCCCTGTACCCAGAAAAGGGGAGCCCTCTGC	208635
Db	207496	GGACTCATCGAGGTGTGGAGGAAGAGGGGAGCTCCCATGACTGCTGACCGCTTCTC	207555	Qy	2040	-----	2040
Qy	1899	-----	1915	Db	208636	CTCTGAGCCCTGCTTGGCCCTAGTTTCATGGCTCCTCTCTGTTGACTGGGATGGCGGA	208695
Db	207556	TCCTCCCGCCAGGTCCACTCCACTCTCTACCCGTTGCGCGGCTGCCACATTCACCT	207615	Qy	2040	-----	2040
Qy	1916	AlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyrProThrLeuMetGluPro	1935	Db	208696	GGCTATAGCCAGCGGGGCCCGGGGACCCAGGGTCACTCCAGGCCACACCCCACTTC	208755
Db	207616	GCCACCCACTGCCCACTGGGCGGCACCTCGATGGGGTCTACCCCTACCTCATGGAGCCC	207675	Qy	2040	-----	2040
Qy	1936	ValLeuLeuProLysGluAlaProArgValAlaArgProGluArgProArgAlaAspThr	1955	Db	208756	TCACTCGCCCCACACACTCTCTCCCGAGAGACCATGCTGCCCTCATCTCACGCTGGCC	208815
Db	207676	GTCTTGCTGCCAAGGAGGCCCGCCGGTGC CGCGGCAGAGCGGCCCGGAGACACC	207735	Qy	2040	-----	2040
Qy	1956	GlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuGluProAlaSerSerPro	1975	Db	208816	TCGCGCGGCTCCACACACTGAACCCATCTCTGTCCCTTCTTGCTTAATCTCTCTCTGTG	208875
Db	207736	GGCCATGCTTCTCGCCCAAGGCCCGCCGGTGC CGCGGCAGAGCGGCCCGGCTCTCCCC	207795	Qy	2040	-----	2040
Qy	1976	SerLysGlySerGluProArgProLeuValProProValSerGlyHisAlaThrIleAla	1995	Db	208876	TCTCCCTCTGTGTCTGTCTGTCCCGGGCTGTGCATCTCTCTCCACTCTCCCTTGCC	208935
Db	207796	AGCAAGGCTCGGAGCCCGGCCCTAGTGCTCTCTCTGTCTGTGGCCAGGCCACATCGCC	207855				

QY	2040	-----	2040
Db	208936	TCCTGTCTCTCCCAACACCCCTCTCTGCTTACTGTCTTTGGGAGCCCAACCCCTACC	208995
QY	2040	-----	2040
Db	208996	CCTAGCTTGGGTTCCCTTGACCCCGGGTCCAGCCAGCTGGGAGGCGACCCCTGC	209055
QY	2041	-----	2041
Db	209056	CCCTGGGCTCCGAACCCCTGGGCGGGTCCGTGACTCTGCACCCCGGCTGCCCTAGG	209115
QY	2042	YTyHisGlySerSerTySerProGluGlyValGluProValSerProValSerSerPr	2062
Db	209116	TTACACGGCAGCAGCTACAGCCCCGAGGGGTGGAGCCGCTCAGCCCTGTGAGCTCACC	209175
QY	2062	oSerLeuThrHisAspLysGlyLeuProLysHisLeuGluGluLeuAspLysSerHisLe	2082
Db	209176	CAGTCTGACCCACGACAAGGGGCTCCCAAGCACCTGGAAGAGCTCGACAAGAGCCACCT	209235
QY	2082	uGluGlyGluLeuArgProLysGlnPro-----	2091
Db	209236	GGAGGGGAGCTGCGGCCCAAGCAGCCAGTAAGCCCCACCCAGTACCCAGGCCCCCGAA	209295
QY	2091	-----	2091
Db	209296	GCCCTGCACAGTGAGGACCTCAAGGCCCATCATGCAGATAGGAAAACAGAGGTGCCTA	209355
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QY	2092	-----	2092
Db	209416	GCAGCCCTGGGGCCAGCAGACACCCCTGACAGCTCTGCTGCTGCGAGGCCCCGTGA	209475
QY	2095	ysLeuGlyGlyGluAlaHisLeuProHisLeuArgProLeuProGluSerGlnProS	2115
Db	209476	AGCTTGGGGGAGGCGGCCACCTCCACACCTGCGGCGCTGCTGCTGAGAGCCAGCCCT	209535
QY	2115	erSerSerProLeuLeuGlnThrAlaProGlyValLysGlyHisGlnArgValThrL	2135
Db	209536	CGTCAGCCCGCTGCTCCAGACCCGCCCGGGTCAAAAGGTCAACAGCGGTGCTCACCC	209595
QY	2135	euaIaGlnHisIleSer-----	2140
Db	209596	TGGCCCAAGACATCAGTGTAACTAGCGGTTCTCTGCTGCTGTGTCAACCTTTGCACCTG	209655
QY	2140	-----	2140
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QY	2140	-----	2140
Db	209716	GCTGGGGATCCAGGGCATGCGCTGGGGGATCCAGGGCTGGGTGAGGTGAGATCCC	209775
QY	2140	-----	2140
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QY	2140	-----	2140
Db	209836	AGCCGATGGCATCTTCAGGGCAATGAGGCTTCTGCTGGGCCAGGTTTCTCAGTGTCA	209895
QY	2140	-----	2140
Db	209896	TGGGCTGTCTCATCAGCCATCTGCCAACTACAGCTTGGAGCCGCTGAOCACAGCCCCA	209955
QY	2140	-----	2140
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QY	2140	-----	2140

Db	210016	GGAAGCTGGCCCCACCCAGGATTCTGCCCGAGCTCCGTCTAGCCCTCCCCACCCCCAG	210075
QY	2141	-----	2141
Db	210076	AAGGTTCTGTAGGAGAGTGCTGCCTGACTTGGGGCCCCCACCCTTGCCTGCGAGGAGTTC	210135
QY	2143	IlleThrGlnAspTyrrThrArgHisHisProGlnGlnLeuSerAlaProLeuProAlaPro	2162
Db	210136	ATCACACAGGACTACACCGGACACCCACACAGCAGCTCAGCGACCCCTGCCGCCCC	210195
QY	2163	LeuTySerPheProGlyAlaSerCysProValLeuAspLeuArgArgProProSerAsp	2182
Db	210196	CTCTACTCTCCCTGGGGCAGCTGCCCGCTCTGGACCTCGCGCGCCACCCAGTGCAC	210255
QY	2183	LeuTyLeuProProProAspHisGlyAlaProAlaAtgGlySerProHisSerGluGly	2202
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Db 211216 TAGCCCGGGCCCTCTGTGTGTACAATTCATGAACCTAAATAAATGATTTTACATTTTAAA 211275
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Db 211276 GGGTTGTTTAAAAAATAAATAATGATTAACGATACATGCCAGAGATTACTTGTGTGTCG 211335
Qy 2204 ----- 2204
Db 211336 ABAATGCTAAACGTTTATGATTTTGGCCACGTACAGGAAAGCGTGTGGGGCCCTGGTT 211395
Qy 2204 ----- 2204
Db 211396 TAGAGTGGAGGAGGTGCGCCCTCTCAGTAGGAGACCTCTGACCACATCTGGGGCCCT 211455
Qy 2205 -----ArgSerProGluProAsnLysThrSerValLeuGlyGlyGluAspG1 2221
Db 211456 TTCTCCATCCAGGTCTCCAGAGCCAAACAAGACGTGCGTCTTGGGTGGTGGTGAGGACGG 211515
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Qy 2255 ----- 2255
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Qy 2256 -----ArgMetGlySerLy 2260
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Qy 2260 sSerProGlyAsnThrSerGlnProProAlaPhePheSerLysLeuThrGluSerAsnSe 2280
Db 212295 GTCTCCAGGCAACACCAGCCAGCCGCGGCTCTTCTTCAGCAAGCTGACCGAGAGCAACTC 212354
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RESULT 17
US-09-920-300A-485
; Sequence 485, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secretair, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121-547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-485

Alignment Scores:
Pred. No.: 4,96e-37 Length: 520
Score: 746.50 Matches: 141
Percent Similarity: 91.95% Conservative: 19
Best Local Similarity: 81.03% Mismatches: 13
Query Match: 5.65% Indels: 1
DB: 9 Gaps: 1

US-09-522-753-5 (1-2517) x US-09-920-300A-485 (1-520)

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Qy 305 LeuMetGluAlaLeuGluLysLysValGluArgIleGluAsnAsnProArgArgAla 324
Db 61 CTATCGAGGCATGGGAGAAAAAAGTGACAGAAATAGAAATAATCTCTCGAGGAAAGCT 120
Qy 325 LysGluSerLysValArgGluTyTrpGluLysGlnPheProGluIleArgLysGlnArg 344
Db 121 AAAGAAGCAAAACAGAGGATCTATGAAGAGCTTTCAGAAATTCGAAACAAGA 180
Qy 345 GluLeuGlnGluArgMetGlnSerArgValGlyGlnArgGlySerGlyLeuSerMetSer 364
Db 181 GAACAGCAAGAAAGATTTCAG---CGAGTTGGGACAGGGGAGCTGCTCTTCAGCCACC 237
Qy 365 AlaAlaArgSerGluHisGluValSerGluIleAspGlyLeuSerGluGlnGluAsn 384
Db 238 ATTGCTGAGGAGTGAAGATTTCTGAAATTTATTTGATGGGCTCTCTGAGCAGGAGAA 297

